

16U 100 PCT.ST25
SEQUENCE LISTING

<110> OriGene Technologies, Inc

<120> NOVEL EXPRESSED GENES

<130> 16U 100 PCT

<150> US 10/112,372

<151> 2002-04-01

<150> US 60/382,614

<151> 2002-05-24

<150> US 10/164,717

<151> 2002-06-10

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<151> 2002-07-30

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Gln Cys Ser Ala Leu Ser Asp Gly Glu Leu Val Tyr Lys Tyr Pro Ser
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Gly Ser Gln Gly Val Leu Thr Glu Ile Lys His Pro Leu Pro Thr Val
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Met Gly Ser Thr Met Glu
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Pro Pro Gly Gly Ala Tyr Leu His Leu Gly Ala Val Thr Ser Pro Val
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Gly Thr Ala Arg Val Leu Gln Leu Ala Phe Gly Cys Thr Thr Phe Ser
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Leu Val Ala His Arg Gly Gly Phe Ala Gly Val Gln Gly Thr Phe Cys
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 Met Pro Glu Pro Trp Gly Thr Val Tyr Phe Leu Gly Ile
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 Ala Gln Val Phe Ser Phe Leu Phe Ser Trp Trp Asn Leu Glu Gly Val
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 Met Asn Gln Ala Asp Ala Pro Arg Pro Leu Asn Trp Thr Ile Arg Lys
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 ctg tgc cac gca gcc ttt ctt cca tct gtc aga ctt ctg aag gct cag 613
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 Lys Ser Trp Ile Glu Arg Ala Phe Tyr Lys Arg Glu Cys Val His Ile
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 Ile Pro Ser Thr Lys Asp Pro His Arg Cys Cys Cys Gly Arg Leu Ile
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 Gly Gln His Val Gly Leu Thr Pro Ser Ile Ser Val Leu Gln Asn Glu
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 Lys Asn Glu Ser Arg Leu Ser Arg Asn Asp Ile Gln Ser Glu Lys Trp
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 Ser Ile Ser Lys His Thr Gln Leu Ser Pro Thr Asp Ala Phe Gly Thr
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ggg ctc atc aaa gca gca atg aca act gga gcg tgg ata ttc act gga Gly Leu Ile Lys Ala Ala Met Thr Thr Gly Ala Trp Ile Phe Thr Gly 210 215 220	1093
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cat gcc tct aag tct cga gga aag ata tgc acc ata ggt att gcc ccc His Ala Ser Lys Ser Arg Gly Lys Ile Cys Thr Ile Gly Ile Ala Pro 240 245 250	1189
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cgg cca tac cag acc atg tcc aat ccc atg agc aag ctc act gtt ctc Arg Pro Tyr Gln Thr Met Ser Asn Pro Met Ser Lys Leu Thr Val Leu 270 275 280 285	1285
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tta gtt ctg gac aga gtg gat ttt gtg aaa tta ctc ata gag aat gga Leu Val Leu Asp Arg Val Asp Phe Val Lys Leu Ile Glu Asn Gly 495 500 505			1957
gta agc atg cac cgt ttt ctc acc atc tcc aga cta gag gaa ttg tac Val Ser Met His Arg Phe Leu Thr Ile Ser Arg Leu Glu Glu Leu Tyr 510 515 520 525			2005
aat acg aga cat ggg ccc tca aat aca ttg tac cac ttg gtc agg gat Asn Thr Arg His Gly Pro Ser Asn Thr Leu Tyr His Leu Val Arg Asp 530 535 540			2053
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tac acg cgc aag cgc ttc cgg acc ctc tac cac aac ctc ttc ggc ccc Tyr Thr Arg Lys Arg Phe Arg Thr Leu Tyr His Asn Leu Phe Gly Pro 575 580 585			2197
aag agg ccc aaa gcc ttg aaa ctg ctg gga atg gag gat gat att ccc Lys Arg Pro Lys Ala Leu Lys Leu Leu Gly Met Glu Asp Asp Ile Pro 590 595 600 605			2245
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gag ctc atg gtg tgg gct gtt ctc atg aag cgg cag aag atg gcc ctg Glu Leu Met Val Trp Ala Val Leu Met Lys Arg Gln Lys Met Ala Leu 640 645 650			2389
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tgc aag ctc tgc aaa gcc atg gct cat gag gcc tct gag aac gac atg Cys Lys Leu Cys Lys Ala Met Ala His Glu Ala Ser Glu Asn Asp Met 670 675 680 685			2485
gtt gac gac att tcc cag gag ctg aat cac aat tcc aga gac ttt ggc Val Asp Asp Ile Ser Gln Glu Leu Asn His Asn Ser Arg Asp Phe Gly 690 695 700			2533
cag ctg gct gtg gag ctc ctg gac cag tcc tac aag cag gac gaa cag Gln Leu Ala Val Glu Leu Leu Asp Gln Ser Tyr Lys Gln Asp Glu Gln 705 710 715			2581
ctg gcc atg aaa ctg ctg acg tat gag ctg aag aac tgg agc aac gcc Leu Ala Met Lys Leu Leu Thr Tyr Glu Leu Lys Asn Trp Ser Asn Ala 720 725 730			2629
acg tgc ctg cag ctt gcc gtg gct gcc aaa cac cgc gac ttc atc gcg Thr Cys Leu Gln Leu Ala Val Ala Ala Lys His Arg Asp Phe Ile Ala 735 740 745			2677
cac acg tgc agc cag atg ctg ctc acc gac atg tgg atg ggc cgg ctc His Thr Cys Ser Gln Met Leu Leu Thr Asp Met Trp Met Gly Arg Leu 750 755 760 765			2725
cgc atg cgc aag aac tca ggc ctc aag gta att ctg gga att cta ctt			2773

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Arg Met Arg Lys Asn Ser Gly Leu Lys Val Ile Leu Gly Ile Leu Leu	770	775	780	
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Pro Pro Ser Ile Leu Ser Leu Glu Phe Lys Asn Lys Asp Asp Met Pro	785	790	795	
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Tyr Met Ser Gln Ala Gln Glu Ile His Leu Gln Glu Lys Glu Ala Glu	800	805	810	
gaa cca gag aag ccc aca aag gaa aaa gag gaa gag gac atg gag ctc				2917
Glu Pro Glu Lys Pro Thr Lys Glu Lys Glu Glu Glu Asp Met Glu Leu	815	820	825	
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Thr Ala Met Leu Gly Arg Asn Asn Gly Glu Ser Ser Arg Lys Lys Asp	830	835	840	845
gaa gag gaa gtt cag agc aag cac cgg tta atc ccc ctc ggc aga aaa				3013
Glu Glu Glu Val Gln Ser Lys His Arg Leu Ile Pro Leu Gly Arg Lys	850	855	860	
atc tat gaa ttc tac aat gca ccc atc gtg aag ttc tgg ttc tac aca				3061
Ile Tyr Glu Phe Tyr Asn Ala Pro Ile Val Lys Phe Trp Phe Tyr Thr	865	870	875	
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Leu Ala Tyr Ile Gly Tyr Leu Met Leu Phe Asn Tyr Ile Val Leu Val	880	885	890	
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Lys Met Glu Arg Trp Pro Ser Thr Gln Glu Trp Ile Val Ile Ser Tyr	895	900	905	
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Ile Phe Thr Leu Gly Ile Glu Lys Met Arg Glu Ile Leu Met Ser Glu	910	915	920	925
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Pro Gly Lys Leu Leu Gln Lys Val Lys Val Trp Leu Gln Glu Tyr Trp	930	935	940	
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Cys Val Asn Ile Ile Tyr Trp Tyr Ile Arg Leu Leu Asp Ile Phe Gly	975	980	985	
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Val Asn Lys Tyr Leu Gly Pro Tyr Val Met Met Ile Gly Lys Met Met	990	995	1000	1005
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Ile Asp Met Met Tyr Phe Val Ile Ile Met Leu Val Val Leu Met	1010	1015	1020	
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Ser Phe Gly Val Ala Arg Gln Ala Ile Leu Phe Pro Asn Glu Glu	1025	1030	1035	
cca tca tgg aaa ctg gcc aag aac atc ttc tac atg ccc tat tgg				3580
Pro Ser Trp Lys Leu Ala Lys Asn Ile Phe Tyr Met Pro Tyr Trp	1040	1045	1050	
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Met Ile Tyr Gly Glu Val Phe Ala Asp Gln Ile Asp Pro Pro Cys	1055	1060	1065	
gga cag aat gag acc cga gag gat ggt aaa ata atc cag ctg cct				3670
Gly Gln Asn Glu Thr Arg Glu Asp Gly Lys Ile Ile Gln Leu Pro	1070	1075	1080	

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Tyr Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala	
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Val Phe Asn Asn Thr Phe Phe Glu Val Lys Ser Ile Ser Asn Gln	
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gtc tgg aag ttt cag agg tat cag ctc atc atg act ttc cat gaa	3850
Val Trp Lys Phe Gln Arg Tyr Gln Leu Ile Met Thr Phe His Glu	
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Arg Pro Val Leu Pro Pro Pro Leu Ile Ile Phe Ser His Met Thr	
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Met Ile Phe Gln His Leu Cys Cys Arg Trp Arg Lys His Glu Ser	
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Glu Tyr Phe Arg Glu Lys Asp Asp Arg Phe Asn Ser Ser Asn Asp	
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Leu Gln Thr Val Asp Ile Arg Leu Ala Gln Leu Glu Asp Leu Ile	
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Gly Arg Met Ala Thr Ala Leu Glu Arg Leu Thr Gly Leu Glu Arg	
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gcc gag tcc aac aaa atc cgc tcg agg acc tcg tca gac tgc acg	4300
Ala Glu Ser Asn Lys Ile Arg Ser Arg Thr Ser Ser Asp Cys Thr	
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gac gcc gcc tac att gtc cgt cag agc agc ttc aac agc cag gaa	4345
Asp Ala Ala Tyr Ile Val Arg Gln Ser Ser Phe Asn Ser Gln Glu	
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Glu Lys Leu Glu Ser Ile Phe Lys Glu Arg Ser Leu Ser Leu His	
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1670 1675 16U 100 PCT.ST25 1680

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 1685 1690 1695

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 1700 1705

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Ala Asp Ala Pro Arg Pro Leu Asn Trp Thr Ile Arg Lys Leu Cys His
 35 40 45

Ala Ala Phe Leu Pro Ser Val Arg Leu Leu Lys Ala Gln Lys Ser Trp
 50 55 60

Ile Glu Arg Ala Phe Tyr Lys Arg Glu Cys Val His Ile Ile Pro Ser
 65 70 75 80

Thr Lys Asp Pro His Arg Cys Cys Cys Gly Arg Leu Ile Gly Gln His
 85 90 95

Val Gly Leu Thr Pro Ser Ile Ser Val Leu Gln Asn Glu Lys Asn Glu
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Ser Arg Leu Ser Arg Asn Asp Ile Gln Ser Glu Lys Trp Ser Ile Ser
 115 120 125

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Lys His Thr Gln Leu Ser Pro Thr Asp Ala Phe Gly Thr Ile Glu Phe
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Gln Gly Gly Gly His Ser Asn Lys Ala Met Tyr Val Arg Val Ser Phe
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Asp Thr Lys Pro Asp Leu Leu Leu His Leu Met Thr Lys Glu Trp Gln
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Leu Glu Leu Pro Lys Leu Leu Ile Ser Val His Gly Gly Leu Gln Asn
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Lys Ala Ala Met Thr Thr Gly Ala Trp Ile Phe Thr Gly Gly Val Asn
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Ala Glu Val Lys Leu Arg Arg Gln Leu Glu Lys His Ile Ser Leu Gln
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Lys Ile Asn Thr Arg Ile Gly Gln Gly Val Pro Val Val Ala Leu Ile
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Val Glu Gly Gly Pro Asn Val Ile Ser Ile Val Leu Glu Tyr Leu Arg
340 345 350

Asp Thr Pro Pro Val Pro Val Val Val Cys Asp Gly Ser Gly Arg Ala
355 360 365

Ser Asp Ile Leu Ala Phe Gly His Lys Tyr Ser Glu Glu Gly Gly Leu
370 375 380

Ile Asn Glu Ser Leu Arg Asp Gln Leu Leu Val Thr Ile Gln Lys Thr
385 390 395 400

Phe Thr Tyr Thr Arg Thr Gln Ala Gln His Leu Phe Ile Ile Leu Met
405 410 415

Glu Cys Met Lys Lys Lys Glu Leu Ile Thr Val Phe Arg Met Gly Ser
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Glu Gly His Gln Asp Ile Asp Leu Ala Ile Leu Thr Ala Leu Leu Lys
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16U 100 PCT.ST25

Gly Ala Asn Ala Ser Ala Pro Asp Gln Leu Ser Leu Ala Leu Ala Trp
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Asn Arg Val Asp Ile Ala Arg Ser Gln Ile Phe Ile Tyr Gly Gln Gln
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Trp Pro Val Gly Ser Leu Glu Gln Ala Met Leu Asp Ala Leu Val Leu
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Asp Arg Val Asp Phe Val Lys Leu Leu Ile Glu Asn Gly Val Ser Met
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His Arg Phe Leu Thr Ile Ser Arg Leu Glu Glu Leu Tyr Asn Thr Arg
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His Gly Pro Ser Asn Thr Leu Tyr His Leu Val Arg Asp Val Lys Lys
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Gly Asn Leu Pro Pro Asp Tyr Arg Ile Ser Leu Ile Asp Ile Gly Leu
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Val Ile Glu Tyr Leu Met Gly Gly Ala Tyr Arg Cys Asn Tyr Thr Arg
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Lys Arg Phe Arg Thr Leu Tyr His Asn Leu Phe Gly Pro Lys Arg Pro
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Lys Ala Leu Lys Leu Leu Gly Met Glu Asp Asp Ile Pro Leu Arg Arg
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Gly Arg Lys Thr Thr Lys Lys Arg Glu Glu Glu Val Asp Ile Asp Leu
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Asp Asp Pro Glu Ile Asn His Phe Pro Phe Pro Phe His Glu Leu Met
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Val Trp Ala Val Leu Met Lys Arg Gln Lys Met Ala Leu Phe Phe Trp
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Gln His Gly Glu Glu Ala Met Ala Lys Ala Leu Val Ala Cys Lys Leu
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Cys Lys Ala Met Ala His Glu Ala Ser Glu Asn Asp Met Val Asp Asp
 675 680 685

Ile Ser Gln Glu Leu Asn His Asn Ser Arg Asp Phe Gly Gln Leu Ala
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Lys Leu Leu Thr Tyr Glu Leu Lys Asn Trp Ser Asn Ala Thr Cys Leu
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Gln Leu Ala Val Ala Ala Lys His Arg Asp Phe Ile Ala His Thr Cys
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Ser Gln Met Leu Leu Thr Asp Met Trp Met Gly Arg Leu Arg Met Arg

16U 100 PCT.ST25
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 785 790 795 800
 Gln Ala Gln Glu Ile His Leu Gln Glu Lys Glu Ala Glu Glu Pro Glu
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 Lys Pro Thr Lys Glu Lys Glu Glu Glu Asp Met Glu Leu Thr Ala Met
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 Val Gln Ser Lys His Arg Leu Ile Pro Leu Gly Arg Lys Ile Tyr Glu
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 Phe Tyr Asn Ala Pro Ile Val Lys Phe Trp Phe Tyr Thr Leu Ala Tyr
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 Ile Gly Tyr Leu Met Leu Phe Asn Tyr Ile Val Leu Val Lys Met Glu
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 Arg Trp Pro Ser Thr Gln Glu Trp Ile Val Ile Ser Tyr Ile Phe Thr
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 Leu Leu Gln Lys Val Lys Val Trp Leu Gln Glu Tyr Trp Asn Val Thr
 930 935 940
 Asp Leu Ile Ala Ile Leu Leu Phe Ser Val Gly Met Ile Leu Arg Leu
 945 950 955 960
 Gln Asp Gln Pro Phe Arg Ser Asp Gly Arg Val Ile Tyr Cys Val Asn
 965 970 975
 Ile Ile Tyr Trp Tyr Ile Arg Leu Leu Asp Ile Phe Gly Val Asn Lys
 980 985 990
 Tyr Leu Gly Pro Tyr Val Met Met Ile Gly Lys Met Met Ile Asp Met
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 Met Tyr Phe Val Ile Ile Met Leu Val Val Leu Met Ser Phe Gly
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 Lys Leu Ala Lys Asn Ile Phe Tyr Met Pro Tyr Trp Met Ile Tyr
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 Gly Glu Val Phe Ala Asp Gln Ile Asp Pro Pro Cys Gly Gln Asn
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16U 100 PCT.ST25

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Thr Gly Ala Trp Ile Val Pro Ala Ile Met Ala Cys Tyr Leu Leu
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 1160 1165 1170

Glu Arg Asp Tyr Gly Leu Lys Leu Phe Ile Thr Asp Asp Glu Leu
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Lys Lys Val His Asp Phe Glu Glu Gln Cys Ile Glu Glu Tyr Phe
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Asn Lys Ile Arg Ser Arg Thr Ser Ser Asp Cys Thr Asp Ala Ala
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Tyr Ile Val Arg Gln Ser Ser Phe Asn Ser Gln Glu Gly Asn Thr
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Phe Lys Leu Gln Glu Ser Ile Asp Pro Ala Gly Glu Glu Thr Met
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Ser Pro Thr Ser Pro Thr Leu Met Pro Arg Met Arg Ser His Ser
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Phe Tyr Ser Val Asn Met Lys Asp Lys Gly Gly Ile Glu Lys Leu
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Glu Ser Ile Phe Lys Glu Arg Ser Leu Ser Leu His Arg Ala Thr
 1355 1360 1365

16U 100 PCT.ST25

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 Cys Ile Asp Ile Tyr Val Ser Ala Met Asp Glu Leu His Cys Asp
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 Pro Ser Phe Ser Thr Pro Val Pro Ser Thr Ala Pro Ser Ser Ser
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 Ala Tyr Ala Thr Leu Ala Pro Thr Asp Arg Pro Pro Ser Arg Ser
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 Ser Asp Tyr Thr His Leu Pro Glu Cys Gln Asn Pro Trp Asp Ser
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 Glu Pro Pro Met Tyr His Thr Ile Glu Arg Ser Lys Ser Ser Arg
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 1565 1570 1575
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 1580 1585 1590
 Ser Ser Asp Ser Glu Glu Asn Glu Ala Lys Gly Arg Arg Ala Thr
 1595 1600 1605
 Ile Ala Ile Ser Ser Gln Glu Gly Asp Asn Ser Glu Arg Thr Leu
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 Ser Asn Asn Ile Thr Val Pro Lys Ile Glu Arg Ala Asn Ser Tyr
 1625 1630 1635
 Ser Ala Glu Glu Pro Ser Ala Pro Tyr Ala His Thr Arg Lys Ser
 1640 1645 1650
 Phe Ser Ile Ser Asp Lys Leu Asp Arg Gln Arg Asn Thr Ala Ser
 1655 1660 1665

16U 100 PCT.ST25

Leu Arg Asn Pro Phe Gln Arg Ser Lys Ser Ser Lys Pro Glu Gly
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 35 40 45

Arg Lys Asn Ser Gly Leu Lys Val Ile Leu Gly Ile Leu Leu Pro Pro
 50 55 60

Ser Ile Leu Ser Leu Glu Phe Lys Asn Lys Asp Asp Met Pro Tyr Met
 65 70 75 80

Ser Gln Ala Gln Glu Ile His Leu Gln Glu Lys Glu Ala Glu Glu Pro
 85 90 95

Glu Lys Pro Thr Lys Glu Lys Glu Glu Glu Asp Met Glu Leu Thr Ala
 100 105 110

Met Leu Gly Arg Asn Asn Gly Glu Ser Ser Arg Lys Lys Asp Glu Glu
 115 120 125

Glu Val Gln Ser Lys His Arg Leu Ile Pro Leu Gly Arg Lys Ile Tyr
 130 135 140

Glu Phe Tyr Asn Ala Pro Ile Val Lys Phe Trp Phe Tyr Thr Leu Ala
 145 150 155 160

Tyr Ile Gly Tyr Leu Met Leu Phe Asn Tyr Ile Val Leu Val Lys Met
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Glu Arg Trp Pro Ser Thr Gln Glu Trp Ile Val Ile Ser Tyr Ile Phe
 180 185 190

Thr Leu Gly Ile Glu Lys Met Arg Glu Ile Leu Met Ser Glu Pro Gly
 195 200 205

Lys Leu Leu Gln Lys Val Lys Val Trp Leu Gln Glu Tyr Trp Asn Val
 210 215 220

Thr Asp Leu Ile Ala Ile Leu Leu Phe Ser Val Gly Met Ile Leu Arg
 225 230 235 240

16U 100 PCT.ST25

Leu Gln Asp Gln Pro Phe Arg Ser Asp Gly Arg Val Ile Tyr Cys Val
 245 250 255

Asn Ile Ile Tyr Trp Tyr Ile Arg Leu Leu Asp Ile Phe Gly Val Asn
 260 265 270

Lys Tyr Leu Gly Pro Tyr Val Met Met Ile Gly Lys Met Met Ile Asp
 275 280 285

Met Met Tyr Phe Val Ile Ile Met Leu Val Val Leu Met Ser Phe Gly
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Val Ala Arg Gln Ala Ile Leu Phe Pro Asn Glu Glu Pro Ser Trp Lys
 305 310 315 320

Leu Ala Lys Asn Ile Phe Tyr Met Pro Tyr Trp Met Ile Tyr Gly Glu
 325 330 335

Val Phe Ala Asp Gln Ile Asp Pro Pro Cys Gly Gln Asn Glu Thr Arg
 340 345 350

Glu Asp Gly Lys Ile Ile Gln Leu Pro Pro Cys Lys Thr Gly Ala Trp
 355 360 365

Ile Val Pro Ala Ile Met Ala Cys Tyr Leu Leu Val Ala Asn Ile Leu
 370 375 380

Leu Val Asn Leu Leu Ile Ala Val Phe Asn Asn Thr Phe Phe Glu Val
 385 390 395 400

Lys Ser Ile Ser Asn Gln Val Trp Lys Phe Gln Arg Tyr Gln Leu Ile
 405 410 415

Met Thr Phe His Glu Arg Pro Val Leu Pro Pro Pro Leu Ile Ile Phe
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Ser His Met Thr Met Ile Phe Gln His Leu Cys Cys Arg Trp Arg Lys
 435 440 445

His Glu Ser Asp Pro Asp Glu Arg Asp Tyr Gly Leu Lys Leu Phe Ile
 450 455 460

Thr Asp Asp Glu Leu Lys Lys Val His Asp Phe Glu Glu Gln Cys Ile
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Glu Glu Tyr Phe Arg Glu Lys Asp Asp Arg Phe Asn Ser Ser Asn Asp
 485 490 495

Glu Arg Ile Arg Val Thr Ser Glu Arg Val Glu Asn Met Ser Met Arg
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Leu Glu Glu Val Asn Glu Arg Glu His Ser Met Lys Ala Ser Leu Gln
 515 520 525

Thr Val Asp Ile Arg Leu Ala Gln Leu Glu Asp Leu Ile Gly Arg Met
 530 535 540

Ala Thr Ala Leu Glu Arg Leu Thr Gly Leu Glu Arg Ala Glu Ser Asn

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16U 100 PCT.ST25

Pro Glu Arg Glu Ala Glu Leu Ser His Pro Ser Ser Asp Ser Glu Glu
865 870 875 880

Asn Glu Ala Lys Gly Arg Arg Ala Thr Ile Ala Ile Ser Ser Gln Glu
885 890 895

Gly Asp Asn Ser Glu Arg Thr Leu Ser Asn Asn Ile Thr Val Pro Lys
900 905 910

Ile Glu Arg Ala Asn Ser Tyr Ser Ala Glu Glu Pro Ser Ala Pro Tyr
915 920 925

Ala His Thr Arg Lys Ser Phe Ser Ile Ser Asp Lys Leu Asp Arg Gln
930 935 940

Arg Asn Thr Ala Ser Leu Arg Asn Pro Phe Gln Arg Ser Lys Ser Ser
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Leu Thr Tyr Glu Leu Lys Asn Trp Ser Asn Ala Thr Cys Leu Gln Leu
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Ala Val Ala Ala Lys His Arg Asp Phe Ile Ala His Thr Cys Ser Gln
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Met Leu Leu Thr Asp Met Trp Met Gly Arg Leu Arg Met Arg Lys Asn
65 70 75 80

Ser Gly Leu Lys Val Ile Leu Gly Ile Leu Leu Pro Pro Ser Ile Leu
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Ser Leu Glu Phe Lys Asn Lys Asp Asp Met Pro Tyr Met Ser Gln Ala
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Gln Glu Ile His Leu Gln Glu Lys Glu Ala Glu Glu Pro Glu Lys Pro
115 120 125

Thr Lys Glu Lys Glu Glu Glu Asp Met Glu Leu Thr Ala Met Leu Gly
130 135 140

Arg Asn Asn Gly Glu Ser Ser Arg Lys Lys Asp Glu Glu Glu Val Gln
145 150 155 160

16U 100 PCT.ST25
 Ser Lys His Arg Leu Ile Pro Leu Gly Arg Lys Ile Tyr Glu Phe Tyr
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 Asn Ala Pro Ile Val Lys Phe Trp Phe Tyr Thr Leu Ala Tyr Ile Gly
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 Tyr Leu Met Leu Phe Asn Tyr Ile Val Leu Val Lys Met Glu Arg Trp
 195 200 205
 Pro Ser Thr Gln Glu Trp Ile Val Ile Ser Tyr Ile Phe Thr Leu Gly
 210 215 220
 Ile Glu Lys Met Arg Glu Ile Leu Met Ser Glu Pro Gly Lys Leu Leu
 225 230 235 240
 Gln Lys Val Lys Val Trp Leu Gln Glu Tyr Trp Asn Val Thr Asp Leu
 245 250 255
 Ile Ala Ile Leu Leu Phe Ser Val Gly Met Ile Leu Arg Leu Gln Asp
 260 265 270
 Gln Pro Phe Arg Ser Asp Gly Arg Val Ile Tyr Cys Val Asn Ile Ile
 275 280 285
 Tyr Trp Tyr Ile Arg Leu Leu Asp Ile Phe Gly Val Asn Lys Tyr Leu
 290 295 300
 Gly Pro Tyr Val Met Met Ile Gly Lys Met Met Ile Asp Met Met Tyr
 305 310 315 320
 Phe Val Ile Ile Met Leu Val Val Leu Met Ser Phe Gly Val Ala Arg
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 Gln Ala Ile Leu Phe Pro Asn Glu Glu Pro Ser Trp Lys Leu Ala Lys
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 Asn Ile Phe Tyr Met Pro Tyr Trp Met Ile Tyr Gly Glu Val Phe Ala
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 Asp Gln Ile Asp Pro Pro Cys Gly Gln Asn Glu Thr Arg Glu Asp Gly
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 Lys Ile Ile Gln Leu Pro Pro Cys Lys Thr Gly Ala Trp Ile Val Pro
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 Ala Ile Met Ala Cys Tyr Leu Leu Val Ala Asn Ile Leu Leu Val Asn
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 Ser Asn Gln Val Trp Lys Phe Gln Arg Tyr Gln Leu Ile Met Thr Phe
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 His Glu Arg Pro Val Leu Pro Pro Pro Leu Ile Ile Phe Ser His Met
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16U 100 PCT.ST25

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Ser Ser Phe Asn Ser Gln Glu Gly Asn Thr Phe Lys Leu Gln Glu Ser
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Ile Asp Pro Ala Gly Glu Glu Thr Met Ser Pro Thr Ser Pro Thr Leu
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Met Pro Arg Met Arg Ser His Ser Phe Tyr Ser Val Asn Met Lys Asp
 645 650 655

Lys Gly Gly Ile Glu Lys Leu Glu Ser Ile Phe Lys Glu Arg Ser Leu
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Ser Leu His Arg Ala Thr Ser Ser His Ser Val Ala Lys Glu Pro Lys
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Ala Pro Ala Ala Pro Ala Asn Thr Leu Ala Ile Val Pro Asp Ser Arg
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Arg Pro Ser Ser Cys Ile Asp Ile Tyr Val Ser Ala Met Asp Glu Leu
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Gly Glu Pro Ser Phe Ser Thr Pro Val Pro Ser Thr Ala Pro Ser Ser
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Ser Ala Tyr Ala Thr Leu Ala Pro Thr Asp Arg Pro Pro Ser Arg Ser
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Ile Asp Phe Glu Asp Ile Thr Ser Met Asp Thr Arg Ser Phe Ser Ser
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Asp Tyr Thr His Leu Pro Glu Cys Gln Asn Pro Trp Asp Ser Glu Pro
 785 790 795 800

16U 100 PCT.ST25

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 Val Lys Thr Ala Glu Tyr Thr Ser Ile Thr Asp Cys Ile Asp Thr Arg
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 Val Pro Ile Met Leu Ser Gln Arg Gly Leu Leu Ala Thr Cys Thr His
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16U 100 PCT.ST25

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Leu Pro Pro Cys Lys Thr Gly Ala Trp Ile Val Pro Ala Ile Met Ala
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Cys Tyr Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala
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Val Phe Asn Asn Thr Phe Phe Glu Val Lys Ser Ile Ser Asn Gln Val
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Trp Lys Phe Gln Arg Tyr Gln Leu Ile Met Thr Phe His Glu Arg Pro
145 150 155 160

Val Leu Pro Pro Pro Leu Ile Ile Phe Ser His Met Thr Met Ile Phe
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Gln His Val Cys Cys Arg Trp Arg Lys His Glu Ser Asp Gln Asp Glu
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Arg Asp Tyr Gly Leu Lys Phe Leu Ile Thr Gly Asp Glu Leu Arg Lys
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Val His Asp Phe Glu Glu Gln Cys Ile Glu Glu Tyr Phe Arg Glu Lys
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Glu His Ser Met Lys Ala Ser Leu Gln Thr Val Asp Ile Arg Leu Ala
260 265 270

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Thr Gly Leu Glu Arg Ala Glu Ser Asn Lys Ile Arg Ser Arg Thr Ser
290 295 300

Ser Asp Cys Thr Asp Ala Ala Tyr Ile Val Arg Gln Ser Ser Phe Asn
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Gly Glu Glu Thr Ile Ser Pro Thr Ser Pro Thr Leu Met Pro Arg Met
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Glu Lys Leu Glu Ser Ile Phe Lys Glu Arg Ser Leu Ser Leu His Arg

370 375 16U 100 PCT.ST25
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Ala Thr Ser Ser His Ser Val Ala Lys Glu Pro Lys Ala Pro Ala Ala
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Glu Pro Leu Asp Asn Ser Met Asn Ile Leu Gly Leu Gly Glu Pro Ser
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 465 470 475 480

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 485 490 495

Leu Pro Glu Cys Gln Asn Pro Trp Asp Thr Asp Pro Pro Thr Tyr His
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Glu Tyr Thr Ser Ile Thr Asp Cys Ile Asp Thr Arg Cys Val Asn Ala
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Pro Gln Ala Ile Ala Asp Arg Ala Thr Phe Pro Gly Gly Leu Gly Asp
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Lys Val Glu Asp Leu Ser Cys Cys His Pro Glu Arg Glu Ala Glu Leu
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Ser His Pro Ser Ser Asp Ser Glu Glu Asn Glu Ala Arg Gly Gln Arg
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Ala Ala Asn Pro Ile Ser Ser Gln Glu Ala Glu Asn Ala Asp Arg Thr
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Leu Ser Asn Asn Ile Thr Val Pro Lys Ile Glu Arg Ala Asn Ser Tyr
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Ser Ala Glu Glu Pro Asn Val Pro Tyr Ala His Thr Arg Lys Ser Phe
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Ser Ile Ser Asp Lys Leu Asp Arg Gln Arg Asn Thr Ala Ser Leu Arg
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16U 100 PCT.ST25

Asn Pro Phe Gln Arg Lys Thr Ile Leu Gln Tyr Thr Pro Asn Lys Leu
690 695 700

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Met Ala Val Gln Gly
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Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser Thr Pro Thr Ala Ile
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Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly Ala Arg Cys Leu Glu

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ctg gtg agc ggg agc aac gtg ctg gag acg gcc gtc atc ctc ctg ctg Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala Val Ile Leu Leu Leu 90 95 100			644
gag gcc ggt gca ctg gtg gcc cgg gct gcg gtg ctg cag cag ctg gac Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val Leu Gln Gln Leu Asp 105 110 115			692
aat gtc act gac gtg atc acc tgc agc tcc atg ctg tcc agc ctc tgc Asn Val Thr Asp Val Ile Thr Cys Ser Ser Met Leu Ser Ser Leu Cys 120 125 130			740
ttc ctg ggc gcc atc gcc gtg gac cgc tac atc tcc atc ttc tac gca Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile Ser Ile Phe Tyr Ala 135 140 145			788
ctg cgc tac cac agc atc gtg acc ctg ccg cgg gcg cgg cga gcc gtt Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg Ala Arg Arg Ala Val 150 155 160 165			836
gcg gcc atc tgg gtg gcc agt gtc gtc ttc agc acg ctc ttc atc gcc Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser Thr Leu Phe Ile Ala 170 175 180			884
tac tac gac cac gtg gcc gtc ctg ctg tgc ctc gtg gtc ttc ttc ctg Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu Val Val Phe Phe Leu 185 190 195		/	932
gct atg ctg gtg ctc atg gcc gtg ctg tac gtc cac atg ctg gcc cgg Ala Met Leu Val Leu Met Ala Val Leu Tyr Val His Met Leu Ala Arg 200 205 210			980
gcc tgc cag cac gcc cag ggc atc gcc cgg ctc cac aag agg cag cgc Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu His Lys Arg Gln Arg 215 220 225			1028
ccg gtc cac cag ggc ttt ggc ctt aaa ggc gct gtc acc ctc acc atc Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala Val Thr Leu Thr Ile 230 235 240 245			1076
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aca ctc atc gtc ctc tgc ccc gag cac ccc acg tgc ggc tgc atc ttc Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr Cys Gly Cys Ile Phe 265 270 275			1172
aag aac ttc aac ctc ttt ctc gcc ctc atc atc tgc aat gcc atc atc Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile Cys Asn Ala Ile Ile 280 285 290			1220
gac ccc ctc atc tac gcc ttc cac agc cag gag ctc cgc agg acg ctc Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu Leu Arg Arg Thr Leu 295 300 305			1268
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tgg gat gtg aag tct ctg ggt gga agt gtg tgc caa gag cta ctc cca Trp Asp Val Lys Ser Leu Gly Gly Ser Val Cys Gln Glu Leu Leu Pro 330 335 340			1364
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Gln	Gln	Pro	Gln	Glu	Lys	Gly	Leu	Cys	Asp	Gln	Lys	Ala	Ser	Ser	Thr	
345								350					355			
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tgc agc agg gcc cca gtc ccc tcc act ctt gac gct gtc cta gct gca	1508															
Cys Ser Arg Ala Pro Val Pro Ser Thr Leu Asp Ala Val Leu Ala Ala																
375 380 385																
gaa gag gcg ggt tcc cag cct tcc ctg tgaccacatg tgacctcagc	1555															
Glu Glu Ala Gly Ser Gln Pro Ser Leu																
390 395																
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tgtgaaaact gcgactgcct gcaggggctt cagctgacct actcgtggg gggcggcacg	2215															
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aacgagggcg tctacgacat ctgcttcgc accctcaagc tggccacgcc cacctacggg	2455															
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cagtaccagg acgccacggc cgaggaagag ggcgagatgt acgaagacga cgaggaggag	3115															
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<210> 26
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 26

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
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Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
 20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
 35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
 50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
 65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
 85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
 100 105 110

Leu Gln Gln Leu Asp Asn Val Thr Asp Val Ile Thr Cys Ser Ser Met
 115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
 130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
 145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
 165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
 180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
 195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
 210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
 225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
 245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
 260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
 275 280 285

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Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
 290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Cys Ser Gln Asp
 305 310 315 320

Arg Ala Leu Val Ser Trp Asp Val Lys Ser Leu Gly Gly Ser Val Cys
 325 330 335

Gln Glu Leu Leu Pro Gln Gln Pro Gln Glu Lys Gly Leu Cys Asp Gln
 340 345 350

Lys Ala Ser Ser Thr Ala Leu Gln Arg Leu Leu Gln Lys Glu Pro Arg
 355 360 365

Gly Arg Thr Ser Arg Cys Ser Arg Ala Pro Val Pro Ser Thr Leu Asp
 370 375 380

Ala Val Leu Ala Ala Glu Glu Ala Gly Ser Gln Pro Ser Leu
 385 390 395

<210> 27
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 27

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
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Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
 20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
 35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
 50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
 65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
 85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
 100 105 110

Leu Gln Gln Leu Asp Asn Val Thr Asp Val Ile Thr Cys Ser Ser Met
 115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
 130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
 145 150 155 160

Ala Arg Gln Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
 165 170 175

16U 100 PCT.ST25

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
 180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
 195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
 210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
 225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
 245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
 260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
 275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
 290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Cys Ser Gln Asp
 305 310 315 320

Arg Ala Leu Val Ser Trp Asp Val Lys Ser Leu Gly Gly Ser Val Cys
 325 330 335

Gln Glu Leu Leu Pro Gln Gln Pro Gln Glu Lys Gly Leu Cys Asp Gln
 340 345 350

Lys Ala Ser Ser Thr Ala Leu Gln Arg Leu Leu Gln Lys Glu Pro Arg
 355 360 365

Gly Arg Thr Ser Arg Cys Ser Arg Ala Pro Val Pro Ser Thr Leu Asp
 370 375 380

Ala Val Leu Ala Ala Glu Glu Ala Gly Ser Gln Pro Ser Leu
 385 390 395

<210> 28
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 28

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
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Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
 20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
 35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
 50 55 60

16U 100 PCT.ST25

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Cys Ser Gln Asp
305 310 315 320

Arg Ala Leu Val Ser Trp Asp Val Lys Ser Leu Gly Gly Ser Val Cys
325 330 335

Gln Glu Leu Leu Pro Gln Gln Pro Gln Glu Lys Gly Leu Cys Asp Gln
340 345 350

Lys Ala Ser Ser Thr Ala Leu Gln Arg Leu Leu Gln Lys Glu Pro Arg
355 360 365

Gly Arg Thr Ser Arg Cys Ser Arg Ala Pro Val Pro Ser Thr Leu Asp
370 375 380

16U 100 PCT.ST25

Ala Val Leu Ala Ala Glu Glu Ala Gly Ser Gln Pro Ser Leu
 385 390 395

<210> 29
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 29

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
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Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
 20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
 35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
 50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
 65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
 85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
 100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
 115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
 130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
 145 150 155 160

Ala Arg Gln Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
 165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
 180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
 195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
 210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
 225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
 245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
 260 265 270

16U 100 PCT.ST25

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
 275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
 290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Cys Ser Gln Asp
 305 310 315 320

Arg Ala Leu Val Ser Trp Asp Val Lys Ser Leu Gly Gly Ser Val Cys
 325 330 335

Gln Glu Leu Leu Pro Gln Gln Pro Gln Glu Lys Gly Leu Cys Asp Gln
 340 345 350

Lys Ala Ser Ser Thr Ala Leu Gln Arg Leu Leu Gln Lys Glu Pro Arg
 355 360 365

Gly Arg Thr Ser Arg Cys Ser Arg Ala Pro Val Pro Ser Thr Leu Asp
 370 375 380

Ala Val Leu Ala Ala Glu Glu Ala Gly Ser Gln Pro Ser Leu
 385 390 395

<210> 30
 <211> 317
 <212> PRT
 <213> Homo sapiens

<400> 30

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
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Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
 20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
 35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
 50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
 65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
 85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
 100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
 115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
 130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
 145 150 155 160

16U 100 PCT.ST25

Ala Arg Gln Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 31
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<212> PRT
<213> Homo sapiens

<400> 31

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Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

16U 100 PCT.ST25

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Cys Ser Gln Asp
305 310 315 320

Arg Ala Leu Val Ser Trp Asp Val Lys Ser Leu Gly Gly Ser Val Cys
325 330 335

Gln Glu Leu Leu Pro Gln Gln Pro Gln Glu Lys Gly Leu Cys Asp Gln
340 345 350

Lys Ala Ser Ser Thr Ala Leu Gln Arg Leu Leu Gln Lys Glu Val Lys
355 360 365

Ser Leu Pro Gln Ala Lys Gly Pro Gly Leu Gln Glu Pro Pro
370 375 380

<210> 32
<211> 22
<212> DNA
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<400> 32
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22

<210> 33
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<212> DNA
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16U 100 PCT.ST25

<400> 33
gctcgtcctt cctctaggct cc 22

<210> 34
<211> 22
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<400> 34
aggaagcagc tcccagttct ga 22

<210> 35
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<400> 35
cttccgcagc ggaaatggcg cgccgcccg ggagggcggg agcagcgctcc 50

<210> 36
<211> 50
<212> DNA
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<400> 36
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<211> 50
<212> DNA
<213> Homo sapiens

<400> 37
aacgactttt taaaacgcag agaaaagctc cattcttccc aggacctcag 50

<210> 38
<211> 7062
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cctagcacca cagacttata cttcgcctgc actttccgtc tttcttctct gggcgccac 180
caaca atg gat ggc aac tcc ctg ctc tcg gta cca agc aac ttg gag tca 230
Met Asp Gly Asn Ser Leu Leu Ser Val Pro Ser Asn Leu Glu Ser
1 5 10 15
tca cgg atg tat gac gtt ttg gaa ccg cag cag ggc aga ggc tgt ggc 278
Ser Arg Met Tyr Asp Val Leu Glu Pro Gln Gln Gly Arg Gly Cys Gly
20 25 30
agc tca gga agc ggc ccg ggg aac tcc atc aca gcc tgt aag aag gtt 326
Ser Ser Gly Ser Gly Pro Gly Asn Ser Ile Thr Ala Cys Lys Lys Val
35 40 45
ctt cgc agc aat agc ctg ctg gag tca aca gac tac tgg ttg cag aat 374
Leu Arg Ser Asn Ser Leu Leu Glu Ser Thr Asp Tyr Trp Leu Gln Asn
50 55 60
cag agg atg ccc tgc caa att ggt ttt gta gaa gac aag tct gaa aac 422
Gln Arg Met Pro Cys Gln Ile Gly Phe Val Glu Asp Lys Ser Glu Asn
65 70 75
tgt gct tct gtc tgc ttt gtg aat ctt gat gtg aac aag gat gaa tgc 470

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Cys	Ala	Ser	Val	Cys	Phe	Val	Asn	Leu	Asp	Val	Asn	Lys	Asp	Glu	Cys			
80					85					90					95			
agc	aca	gag	cac	ctg	caa	cag	aaa	ctg	gtc	aac	gtt	tca	cca	gat	ctt			518
Ser	Thr	Glu	His	Leu	Gln	Gln	Lys	Leu	Val	Asn	Val	Ser	Pro	Asp	Leu			
				100					105						110			
cca	aaa	ctt	atc	agt	tcc	atg	aat	gtc	caa	caa	cca	aaa	gaa	aat	gaa			566
Pro	Lys	Leu	Ile	Ser	Ser	Met	Asn	Val	Gln	Gln	Pro	Lys	Glu	Asn	Glu			
				115				120						125				
att	gtt	gtc	cta	agt	ggg	tta	gcc	tct	gga	aat	ctc	cag	gca	gat	ttt			614
Ile	Val	Val	Leu	Ser	Gly	Leu	Ala	Ser	Gly	Asn	Leu	Gln	Ala	Asp	Phe			
				130				135					140					
gaa	gtt	tca	cag	tgc	cct	tgg	ctg	cca	gat	atc	tgc	ttg	gtc	caa	tgt			662
Glu	Val	Ser	Gln	Cys	Pro	Trp	Leu	Pro	Asp	Ile	Cys	Leu	Val	Gln	Cys			
				145			150				155							
gca	aga	ggg	aac	aga	cca	aac	agt	acc	aac	tgc	atc	atc	ttt	gaa	atc			710
Ala	Arg	Gly	Asn	Arg	Pro	Asn	Ser	Thr	Asn	Cys	Ile	Ile	Phe	Glu	Ile			
					165					170				175				
aac	aaa	ttt	ctg	att	ggg	ctg	gaa	ctg	gtg	cag	gag	cga	cag	ctc	cac			758
Asn	Lys	Phe	Leu	Ile	Gly	Leu	Glu	Leu	Val	Gln	Glu	Arg	Gln	Leu	His			
				180					185					190				
ctg	gaa	aca	aac	atc	ttg	aaa	ctg	gag	gat	gac	acg	aac	tgt	tcc	tta			806
Leu	Glu	Thr	Asn	Ile	Leu	Lys	Leu	Glu	Asp	Asp	Thr	Asn	Cys	Ser	Leu			
				195				200						205				
tct	tca	atc	gag	gaa	gac	ttt	ctc	acc	gct	tct	gag	cac	ttg	gag	gag			854
Ser	Ser	Ile	Glu	Glu	Asp	Phe	Leu	Thr	Ala	Ser	Glu	His	Leu	Glu	Glu			
				210			215					220						
gaa	agc	gag	gtg	gat	gaa	tct	agg	aac	gat	tat	gaa	aat	ata	aat	gtc			902
Glu	Ser	Glu	Val	Asp	Glu	Ser	Arg	Asn	Asp	Tyr	Glu	Asn	Ile	Asn	Val			
				225			230				235							
tca	gcc	aat	gtt	ttg	gaa	agt	aaa	cag	cta	aag	gga	gcc	acc	cag	gtg			950
Ser	Ala	Asn	Val	Leu	Glu	Ser	Lys	Gln	Leu	Lys	Gly	Ala	Thr	Gln	Val			
				240		245				250				255				
gaa	tgg	aat	tgc	aac	aag	gaa	aag	tgg	ctt	tat	gct	ttg	gaa	gac	aaa			998
Glu	Trp	Asn	Cys	Asn	Lys	Glu	Lys	Trp	Leu	Tyr	Ala	Leu	Glu	Asp	Lys			
				260				265						270				
tac	atc	aac	aaa	tat	ccc	aca	cca	ttg	att	aaa	aca	gaa	cga	tct	cca			1046
Tyr	Ile	Asn	Lys	Tyr	Pro	Thr	Pro	Leu	Ile	Lys	Thr	Glu	Arg	Ser	Pro			
				275				280						285				
gaa	aac	cta	aca	aag	aac	aca	gcc	ttg	cag	agt	cta	gat	ccc	tca	gcc			1094
Glu	Asn	Leu	Thr	Lys	Asn	Thr	Ala	Leu	Gln	Ser	Leu	Asp	Pro	Ser	Ala			
				290			295						300					
aag	cca	tca	cag	tgg	aaa	aga	gaa	gct	gtg	ggg	aat	ggg	aga	caa	gcc			1142
Lys	Pro	Ser	Gln	Trp	Lys	Arg	Glu	Ala	Val	Gly	Asn	Gly	Arg	Gln	Ala			
				305			310				315							
aca	cat	tat	tat	cat	tca	gaa	gct	ttt	aaa	ggg	caa	atg	gaa	aaa	tca			1190
Thr	His	Tyr	Tyr	His	Ser	Glu	Ala	Phe	Lys	Gly	Gln	Met	Glu	Lys	Ser			
					325				330					335				
cag	gca	ctg	tat	att	cca	aaa	gat	gct	tat	ttc	tcc	atg	atg	gat	aaa			1238
Gln	Ala	Leu	Tyr	Ile	Pro	Lys	Asp	Ala	Tyr	Phe	Ser	Met	Met	Asp	Lys			
				340					345					350				
gat	gta	cct	tct	gca	tgt	gct	gtg	gca	gag	cag	aga	agc	aac	cta	aac			1286
Asp	Val	Pro	Ser	Ala	Cys	Ala	Val	Ala	Glu	Gln	Arg	Ser	Asn	Leu	Asn			
				355				360						365				
cca	gga	gac	cat	gaa	gac	aca	aga	aac	gct	ctc	cct	cct	aga	caa	gat			1334
Pro	Gly	Asp	His	Glu	Asp	Thr	Arg	Asn	Ala	Leu	Pro	Pro	Arg	Gln	Asp			
				370				375					380					
gga	gaa	gtc	acc	act	ggc	aag	tat	gct	aca	aat	tta	gca	gaa	tcc	gtg			1382
Gly	Glu	Val	Thr	Thr	Gly	Lys	Tyr	Ala	Thr	Asn	Leu	Ala	Glu	Ser	Val			
					385			390										

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ctg cag gat gca ttt att aga tta tct caa tct cag tcc aca tta ccc Leu Gln Asp Ala Phe Ile Arg Leu Ser Gln Ser Gln Ser Thr Leu Pro 400 405 410 415	1430
cag gaa tct gca gtc agt gtt tct gta gga agt tct ctg ctt ccc agt Gln Glu Ser Ala Val Ser Val Ser Val Gly Ser Ser Leu Leu Pro Ser 420 425 430	1478
tgc tat tcc aca aaa gat aca gtg gtt tct cgg tca tgg aat gag ctc Cys Tyr Ser Thr Lys Asp Thr Val Val Ser Arg Ser Trp Asn Glu Leu 435 440 445	1526
ccc aaa atc gtc gtt gtt cag agt cca gat ggc agt gat gct gcc cca Pro Lys Ile Val Val Val Gln Ser Pro Asp Gly Ser Asp Ala Ala Pro 450 455 460	1574
cag cca ggc atc tcc tcc tgg cct gag atg gaa gtc tct gtt gaa acc Gln Pro Gly Ile Ser Ser Trp Pro Glu Met Glu Val Ser Val Glu Thr 465 470 475	1622
tca agc atc ctc tct gga gag aac tcc agc aga caa ccc cag agt gct Ser Ser Ile Leu Ser Gly Glu Asn Ser Ser Arg Gln Pro Gln Ser Ala 480 485 490 495	1670
cta gaa gtg gcg tta gct tgt gca gcc act gtg att gga act att tcc Leu Glu Val Ala Leu Ala Cys Ala Ala Thr Val Ile Gly Thr Ile Ser 500 505 510	1718
agt cca cag gcc aca gaa aga ctc aaa atg gag caa gtg gtc tcg aac Ser Pro Gln Ala Thr Glu Arg Leu Lys Met Glu Gln Val Val Ser Asn 515 520 525	1766
ttt ccc cca ggg agc agt ggt gca ctg caa act caa gca ccc caa gga Phe Pro Pro Gly Ser Ser Gly Ala Leu Gln Thr Gln Ala Pro Gln Gly 530 535 540	1814
ctc aag gaa cct tcc atc aat gag tac tcc ttt cca tct gct ttg tgt Leu Lys Glu Pro Ser Ile Asn Glu Tyr Ser Phe Pro Ser Ala Leu Cys 545 550 555	1862
ggc atg act cag gtg gcc agt gcc gtg gct gtc tgt ggt ctg ggt gaa Gly Met Thr Gln Val Ala Ser Ala Val Ala Val Cys Gly Leu Gly Glu 560 565 570 575	1910
aga gaa gag gtg aca tgc tca gtg gct cca agt ggt agc ctc ccg cct Arg Glu Glu Val Thr Cys Ser Val Ala Pro Ser Gly Ser Leu Pro Pro 580 585 590	1958
gca gct gag gct tct gaa gcc atg ccc cca ctt tgt ggt tta gca agc Ala Ala Glu Ala Ser Glu Ala Met Pro Pro Leu Cys Gly Leu Ala Ser 595 600 605	2006
atg gag ctt ggc aag gaa gcc att gcc gag gga ttg ctc aag gag gct Met Glu Leu Gly Lys Glu Ala Ile Ala Glu Gly Leu Leu Lys Glu Ala 610 615 620	2054
gct ctg gtt tta aca agg cct aat acc tac agc agc att gga gac ttt Ala Leu Val Leu Thr Arg Pro Asn Thr Tyr Ser Ser Ile Gly Asp Phe 625 630 635	2102
ctg gac tcc atg aac agg aga atc atg gaa act gct tca aag tct cag Leu Asp Ser Met Asn Arg Arg Ile Met Glu Thr Ala Ser Lys Ser Gln 640 645 650 655	2150
acc ctg tgc tca gaa aat gtc gtc agg aat gaa ctg gca cat acc ctg Thr Leu Cys Ser Glu Asn Val Val Arg Asn Glu Leu Ala His Thr Leu 660 665 670	2198
tcc aat gtt atc ctg agg cat tcc att gat gaa gtt cac cac aaa aat Ser Asn Val Ile Leu Arg His Ser Ile Asp Glu Val His His Lys Asn 675 680 685	2246
atg ata atc gac ccc aat gac aac agg cat tca tct gaa att ctg gac Met Ile Ile Asp Pro Asn Asp Asn Arg His Ser Ser Glu Ile Leu Asp 690 695 700	2294
acc tta atg gaa agt aca aat caa ctg ctt tta gat gtg ata tgc ttc Thr Leu Met Glu Ser Thr Asn Gln Leu Leu Leu Asp Val Ile Cys Phe 705 710 715	2342

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acg ttc aag aag atg agt cat att gta cgg ctt ggt gaa tgt cct gct Thr Phe Lys Lys Met Ser His Ile Val Arg Leu Gly Glu Cys Pro Ala 720 725 730 735	2390
gtc ctt tct aag gag acc atc aga agg agg gag aca gaa cca agc tgc Val Leu Ser Lys Glu Thr Ile Arg Arg Arg Glu Thr Glu Pro Ser Cys 740 745 750	2438
cag cca tct gat ccg ggt gct agt caa gct tgg aca aaa gcc act gaa Gln Pro Ser Asp Pro Gly Ala Ser Gln Ala Trp Thr Lys Ala Thr Glu 755 760 765	2486
tcc tcc agc agc tct cca ctt agc aat tca cac aac acg agt ctt gtc Ser Ser Ser Ser Ser Pro Leu Ser Asn Ser His Asn Thr Ser Leu Val 770 775 780	2534
atc aac aat ctt gtg gat ggc atg tat tca aaa caa gac aag ggt gga Ile Asn Asn Leu Val Asp Gly Met Tyr Ser Lys Gln Asp Lys Gly Gly 785 790 795	2582
gtg agg cca ggc ctc ttc aag aac ccc acg ctg cag tca caa tta tca Val Arg Pro Gly Leu Phe Lys Asn Pro Thr Leu Gln Ser Gln Leu Ser 800 805 810 815	2630
cgt agt cac aga gtg ccc gat tct tca act gct aca aca tcc tcc aag Arg Ser His Arg Val Pro Asp Ser Ser Thr Ala Thr Thr Ser Ser Lys 820 825 830	2678
gaa ata tat ctg aaa gga ata gca gga gag gat aca aaa agc cct cat Glu Ile Tyr Leu Lys Gly Ile Ala Gly Glu Asp Thr Lys Ser Pro His 835 840 845	2726
cac agt gag aat gaa tgc aga gcc tct tcc gaa gga caa agg tcc cca His Ser Glu Asn Glu Cys Arg Ala Ser Ser Glu Gly Gln Arg Ser Pro 850 855 860	2774
acg gtc agc cgg tcc aga agt ggt tcc cag gag gct gag gag agt atc Thr Val Ser Arg Ser Arg Ser Gly Ser Gln Glu Ala Glu Glu Ser Ile 865 870 875	2822
cac cca aac acc caa gaa aag tac aac tgt gcc aca tct cgc atc aac His Pro Asn Thr Gln Glu Lys Tyr Asn Cys Ala Thr Ser Arg Ile Asn 880 885 890 895	2870
gaa gtt caa gtc aac ctg tcc ttg tta ggg gat gac ctg ctg ctt cct Glu Val Gln Val Asn Leu Ser Leu Leu Gly Asp Asp Leu Leu Leu Pro 900 905 910	2918
gct caa tcc acg ctt caa aca aag cat cca gac atc tac tgc att aca Ala Gln Ser Thr Leu Gln Thr Lys His Pro Asp Ile Tyr Cys Ile Thr 915 920 925	2966
gac ttt gcg gaa gaa tta gca gac acg gtc gtc tcc atg gca act gaa Asp Phe Ala Glu Glu Leu Ala Asp Thr Val Val Ser Met Ala Thr Glu 930 935 940	3014
att gca gcg att tgc ctt gac aac tcc agt gga aaa caa ccc tgg ttt Ile Ala Ala Ile Cys Leu Asp Asn Ser Ser Gly Lys Gln Pro Trp Phe 945 950 955	3062
tgt gca tgg aaa aga ggg agt gag ttt ctg atg aca ccc aac gta ccc Cys Ala Trp Lys Arg Gly Ser Glu Phe Leu Met Thr Pro Asn Val Pro 960 965 970 975	3110
tgc cga tcc ttg aag agg aag aaa gag agc cag ggg agc ggg acc gct Cys Arg Ser Leu Lys Arg Lys Lys Glu Ser Gln Gly Ser Gly Thr Ala 980 985 990	3158
gtg agg aaa cac aag cct ccc cgg ctc agt gag atc aag agg aag acg Val Arg Lys His Lys Pro Pro Arg Leu Ser Glu Ile Lys Arg Lys Thr 995 1000 1005	3206
gac gag cac cct gag ctt aaa gaa aag ctg atg aac agg gtt gtg Asp Glu His Pro Glu Leu Lys Glu Lys Leu Met Asn Arg Val Val 1010 1015 1020	3251
gat gag tcc atg aac ctt gaa gat gtc cca gat tct gtc aat ctt Asp Glu Ser Met Asn Leu Glu Asp Val Pro Asp Ser Val Asn Leu	3296

1025	1030	16U 100 PCT.ST25 1035	
ttt gcc aat gaa gtg gca gcc aag atc atg aac cta acg gag ttc Phe Ala Asn Glu Val Ala Ala Lys Ile Met Asn Leu Thr Glu Phe 1040 1045 1050			3341
tct atg gtg gac ggc atg tgg cag gcg cag ggc tat ccc cgg aat Ser Met Val Asp Gly Met Trp Gln Ala Gln Gly Tyr Pro Arg Asn 1055 1060 1065			3386
cgg tta ctg agt ggc gac agg tgg agc cgg ctg aag gcc tcc agc Arg Leu Leu Ser Gly Asp Arg Trp Ser Arg Leu Lys Ala Ser Ser 1070 1075 1080			3431
tgc gaa agc att cct gag gaa gac tcc gag gcc agg gcc tat gtc Cys Glu Ser Ile Pro Glu Glu Asp Ser Glu Ala Arg Ala Tyr Val 1085 1090 1095			3476
aac agc ctg ggc tta atg agc acg ctg agc cag ccg gtc agc agg Asn Ser Leu Gly Leu Met Ser Thr Leu Ser Gln Pro Val Ser Arg 1100 1105 1110			3521
gcc agc tct gtc tcc aag cag tcc agc tgt gag agc atc acc gat Ala Ser Ser Val Ser Lys Gln Ser Ser Cys Glu Ser Ile Thr Asp 1115 1120 1125			3566
gag ttt tcc agg ttc atg gtg aac cag atg gaa aat gaa ggg aga Glu Phe Ser Arg Phe Met Val Asn Gln Met Glu Asn Glu Gly Arg 1130 1135 1140			3611
gga ttt gag tta ctg ctg gat tac tat gct ggc aag aac gcc agc Gly Phe Glu Leu Leu Leu Asp Tyr Tyr Ala Gly Lys Asn Ala Ser 1145 1150 1155			3656
agc att ctg aac tca gcc atg caa cag gcg tgc cgg aaa agt gac Ser Ile Leu Asn Ser Ala Met Gln Gln Ala Cys Arg Lys Ser Asp 1160 1165 1170			3701
cac ctg agt gtg agg cct agc tgt ccc tct aag cag tcc agc aca His Leu Ser Val Arg Pro Ser Cys Pro Ser Lys Gln Ser Ser Thr 1175 1180 1185			3746
gag agc atc act gag gag ttc tac agg tac atg ctg agg gac atc Glu Ser Ile Thr Glu Glu Phe Tyr Arg Tyr Met Leu Arg Asp Ile 1190 1195 1200			3791
gaa aga gac agc aga gaa agt gcc tcc tcc aga cgg agc agc cag Glu Arg Asp Ser Arg Glu Ser Ala Ser Ser Arg Arg Ser Ser Gln 1205 1210 1215			3836
gat tgg aca gcc ggc ctg ctg tct cct tct ctg cga tcc cca gtg Asp Trp Thr Ala Gly Leu Leu Ser Pro Ser Leu Arg Ser Pro Val 1220 1225 1230			3881
tgc cac aga cag tgc tcc atg cca gac agc aga tcc cca tgc tcc Cys His Arg Gln Ser Ser Met Pro Asp Ser Arg Ser Pro Cys Ser 1235 1240 1245			3926
agg ctg aca gtg aat gtg ccc atc aaa gcc aac tct tta gat ggc Arg Leu Thr Val Asn Val Pro Ile Lys Ala Asn Ser Leu Asp Gly 1250 1255 1260			3971
ttt gct cag aac tgc cca caa gat ttc cta agc gtg cag ccg gtc Phe Ala Gln Asn Cys Pro Gln Asp Phe Leu Ser Val Gln Pro Val 1265 1270 1275			4016
agt agc gcg tcc tca tcc ggt ctc tgc aaa tct gac tct tgc ttg Ser Ser Ala Ser Ser Ser Gly Leu Cys Lys Ser Asp Ser Cys Leu 1280 1285 1290			4061
tat cgg aga ggt ggg act gac cac atc acc aac atg tta att cat Tyr Arg Arg Gly Gly Thr Asp His Ile Thr Asn Met Leu Ile His 1295 1300 1305			4106
gaa acg tgg gct agc tcc att gag gct ctc atg cgc aag aac aaa Glu Thr Trp Ala Ser Ser Ile Glu Ala Leu Met Arg Lys Asn Lys 1310 1315 1320			4151
atc att gtg gat gat gca gag gaa gct gac act gag cct gtt tct			4196

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Ile Ile Val	Asp Asp Ala Glu Glu	Ala Asp Thr Glu Pro	Val Ser										
1325	1330	1335											
ggt ggc tct	ccc tcg caa gca gag	aag tgt gca aat aga	tta gct	4241									
Gly Gly Ser	Pro Ser Gln Ala Glu	Lys Cys Ala Asn Arg	Leu Ala										
1340	1345	1350											
gcg agc agg	atg tgc agt ggg cca	act ctg ctt gtt cag	gag tct	4286									
Ala Ser Arg	Met Cys Ser Gly Pro	Thr Leu Leu Val Gln	Glu Ser										
1355	1360	1365											
ctc gat tgc	ccg agg aaa gac tct	ggt acc gaa tgt aaa	cag ccc	4331									
Leu Asp Cys	Pro Arg Lys Asp Ser	Val Thr Glu Cys Lys	Gln Pro										
1370	1375	1380											
cca gtg tca	tct ttg agc aaa act	gct tct ctt aca aac	cac agc	4376									
Pro Val Ser	Ser Leu Ser Lys Thr	Ala Ser Leu Thr Asn	His Ser										
1385	1390	1395											
cct tta gat	tct aaa aaa gaa act	tcc tcg tgc cag gac	cct gta	4421									
Pro Leu Asp	Ser Lys Lys Glu Thr	Ser Ser Cys Gln Asp	Pro Val										
1400	1405	1410											
cca ata aac	cac aaa agg cga tca	ctt tgc tcg agg gaa	gtg cct	4466									
Pro Ile Asn	His Lys Arg Arg Ser	Leu Cys Ser Arg Glu	Val Pro										
1415	1420	1425											
ttg att cag	att gaa aca gat cag	aga gaa gcc tgt gct	ggg gaa	4511									
Leu Ile Gln	Ile Glu Thr Asp Gln	Arg Glu Ala Cys Ala	Gly Glu										
1430	1435	1440											
cct gaa ccc	ttc ctt tcc aaa agc	agc ctc cta gag gaa	gca gaa	4556									
Pro Glu Pro	Phe Leu Ser Lys Ser	Ser Leu Leu Glu Glu	Ala Glu										
1445	1450	1455											
ggg cat tcg	aat gac aaa aac atc	cca gat gtg gtg aga	ggt gga	4601									
Gly His Ser	Asn Asp Lys Asn Ile	Pro Asp Val Val Arg	Gly Gly										
1460	1465	1470											
gac aca gcc	gtg agc gct tgt caa	atc cat agt gac agc	ctt' gat	4646									
Asp Thr Ala	Val Ser Ala Cys Gln	Ile His Ser Asp Ser	Leu Asp										
1475	1480	1485											
acc aga gat	gta cca gag gct gaa	gcc tcc aca gaa gcc	aga gcc	4691									
Thr Arg Asp	Val Pro Glu Ala Glu	Ala Ser Thr Glu Ala	Arg Ala										
1490	1495	1500											
ccc gat gag	gcc ccc aac cct cca	agc agc agc gag gag	agc aca	4736									
Pro Asp Glu	Ala Pro Asn Pro Pro	Ser Ser Ser Glu Glu	Ser Thr										
1505	1510	1515											
ggc agc tgg	acc cag ctt gcc aat	gag gaa gac aac cca	gat gac	4781									
Gly Ser Trp	Thr Gln Leu Ala Asn	Glu Glu Asp Asn Pro	Asp Asp										
1520	1525	1530											
aca agt agc	ttt ctc cag ctc agt	gag cga tcc atg agc	aat ggc	4826									
Thr Ser Ser	Phe Leu Gln Leu Ser	Glu Arg Ser Met Ser	Asn Gly										
1535	1540	1545											
aac agt agt	gcc act agc agt ctt	ggc att atg gat ctg	gac att	4871									
Asn Ser Ser	Ala Thr Ser Ser Leu	Gly Ile Met Asp Leu	Asp Ile										
1550	1555	1560											
tat cag gaa	agc atg cca tct tct	ccc atg att aat gaa	tta gta	4916									
Tyr Gln Glu	Ser Met Pro Ser Ser	Pro Met Ile Asn Glu	Leu Val										
1565	1570	1575											
gaa gaa aag	aag att ctt aaa gga	cag tca gaa agc aca	gag gca	4961									
Glu Glu Lys	Lys Ile Leu Lys Gly	Gln Ser Glu Ser Thr	Glu Ala										
1580	1585	1590											
cct gca tct	gga ccg cct acg gga	aca gcc agc ccc cag	agg agc	5006									
Pro Ala Ser	Gly Pro Pro Thr Gly	Thr Ala Ser Pro Gln	Arg Ser										
1595	1600	1605											
ctg ctg gtg	atc aac ttt gac ctg	gag cca gag tgt cca	gat gcc	5051									
Leu Leu Val	Ile Asn Phe Asp Leu	Glu Pro Glu Cys Pro	Asp Ala										
1610	1615	1620											

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gag ctc cga gcc act ctg cag tgg	ata gct gcc tct gaa ctg ggg	5096
Glu Leu Arg Ala Thr Leu Gln Trp	Ile Ala Ala Ser Glu Leu Gly	
1625	1635	
att ccc acc atc tac ttt aag aaa	tct cag gaa aac aga att gaa	5141
Ile Pro Thr Ile Tyr Phe Lys Lys	Ser Gln Glu Asn Arg Ile Glu	
1640	1650	
aag ttt cta gat gtc gtg cag ctg	gtt cat cgg aag tcc tgg aaa	5186
Lys Phe Leu Asp Val Val Gln Leu	Val His Arg Lys Ser Trp Lys	
1655	1665	
gtg ggt gat atc ttc cat gca gtt	gtc cag tac tgc aaa atg cat	5231
Val Gly Asp Ile Phe His Ala Val	Val Gln Tyr Cys Lys Met His	
1670	1680	
gag gag cag aag gat ggg aga ctg	agt ctc ttt gac tgg ctc ttg	5276
Glu Glu Gln Lys Asp Gly Arg Leu	Ser Leu Phe Asp Trp Leu Leu	
1685	1695	
gaa ctg gga taa taaggcagtc tgccgtatag atcattcctt ccctttattc		5328
Glu Leu Gly		
1700		
caacttagat tacagtgtt tgttctaaat gctctaaaca ttctcaaaac atcacatcac		5388
attagcagaa ctataaaaaa aaatctgcta ctcagatcca ctgcatacag aataagtcag		5448
aggaaaagca aaatataggt ctgtccaaat tcatacaact tgtgggtgag ttccaaagag		5508
cttggttag aagggtgga caaagagaga attcaatggg gcccaatta gaatgcttat		5568
aatgagaccc aatctccagg aaaacaacac tcacataagt ttaatcatat aaaatgattt		5628
gtaatgtctc taatttagatg aatcaactag aaacaaactc agtgggtcaaa ataattttta		5688
agagtattcc gtaacctata ttttactttt ctgattatat taaggggctg ccagcccga		5748
gaaatactta agatatgggt gagaaatccc cagactttta taaaaagat ttccactttc		5808
aaatcaatgt cagtagacat tgataaaagt atagcagcat cctctactga ggtgatttca		5868
tttattccct gcagcccact gataaatatc tcacttctcc caaatagtat gtggactccc		5928
agctaagcag aaaactattg tcattcaact gaagaggaag ataaaagatt gtcttgtttc		5988
catcactgta ttacttgtgt aacatgatta cataattcctt atcctaagag aaagctttca		6048
tatttaaaaa aaagtctttt cagataaaat ctgcttgtgt cttgaataat atgaaataca		6108
aactttcact ttattttatt gtaaattata aagagattat tgtcttaaat aatatattga		6168
gttagcttca agcttcctaa aatatgaaga gattgtgtgc taaagtcaca tattgacatt		6228
gagctcagt gcctgtttca tcacgtatgt gctgctacct gtacagcaga catgccgctc		6288
cagtgcatt tataatgaca gaagcagggt aatggtcttg tgtttgacat gatcagttag		6348
gatcatagac tttccctgac tcgtagatat tagccttgaa ttgggggaaa agaagacttt		6408
gacacatttt agttatttta ataacagaga tttactcttt tgaaaaataa aggtatctaa		6468
tgtctcccta ataagtcttc tttccttcca actaaatgac ctacacggac ttttattttc		6528
ttgatcaag aggtgtttat taaggacttc tggataacta tacttttact ctatttttaa		6588
agatcacaaa gtaattttta atgtgaacag gttcccatac catgaatgct ggcctcacct		6648
tctctatcat ccacattttg aaatgcaaag aaagctccct tgtaagccat acttccttcc		6708
ccactcccat cctaggatac ttgccagtg ctcattaggc atttcttatt cagatagtcc		6768
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ccatcaattc acgctgaaat gtgcttcttt gtgctatcaa atggaataga atacacttat		6888
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16U 100 PCT.ST25

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16U 100 PCT.ST25

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16U 100 PCT.ST25

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16U 100 PCT.ST25

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Cys Ser Glu Asn Val Val Arg Asn Glu Leu Ala His Thr Leu Ser Asn
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Val Ile Leu Arg His Ser Ile Asp Glu Val His His Lys Asn Met Ile

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16U 100 PCT.ST25

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Phe	Gly	Gln	Met	Thr	Leu	Ser	Arg	Gln	Ser	Ser	Gly	Glu	Thr	Pro	Glu		
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ccc	cca	tca	ggt	cct	gtc	tac	cca	tcc	tcc	ctt	atg	cca	cag	ccg	gcc	2115	
Pro	Pro	Ser	Gly	Pro	Val	Tyr	Pro	Ser	Ser	Leu	Met	Pro	Gln	Pro	Ala		
			610					615						620			
cag	cag	ccc	agc	tat	gta	atc	gcc	tct	aca	ggc	cag	cag	ctt	cct	aca	2163	
Gln	Gln	Pro	Ser	Tyr	Val	Ile	Ala	Ser	Thr	Gly	Gln	Gln	Leu	Pro	Thr		
				625			630							635			
gga	gga	ttc	tca	ggc	tct	ggc	cct	ccc	atc	tcc	cag	cag	gtc	ctc	cag	2211	
Gly	Gly	Phe	Ser	Gly	Ser	Gly	Pro	Pro	Ile	Ser	Gln	Gln	Val	Leu	Gln		
		640				645					650						
ccc	cct	ccc	tca	cca	cag	gga	ttt	gtg	caa	cag	cct	ccg	cct	gca	cag	2259	
Pro	Pro	Pro	Ser	Pro	Gln	Gly	Phe	Val	Gln	Gln	Pro	Pro	Pro	Pro	Ala	Gln	
					660					665					670		
atg	cct	gta	tat	tat	tac	cca	tct	ggt	cag	tac	cct	acc	tca	acc	acg	2307	
Met	Pro	Val	Tyr	Tyr	Tyr	Pro	Ser	Gly	Gln	Tyr	Pro	Thr	Ser	Thr	Thr		
					675					680					685		
caa	cag	tac	cgg	ccc	atg	gcc	ccg	gtt	cag	tac	aac	gct	cag	agg	agt	2355	
Gln	Gln	Tyr	Arg	Pro	Met	Ala	Pro	Val	Gln	Tyr	Asn	Ala	Gln	Arg	Ser		
			690					695						700			
caa	cag	atg	cca	cag	gca	gca	cag	caa	gca	ggt	tac	cag	cca	gtc	ttg	2403	
Gln	Gln	Met	Pro	Gln	Ala	Ala	Gln	Gln	Ala	Gly	Tyr	Gln	Pro	Val	Leu		
			705					710						715			
tct	ggt	caa	cag	gga	ttc	caa	ggc	cta	ata	gga	gtg	cag	cag	cca	cct	2451	
Ser	Gly	Gln	Gln	Gly	Phe	Gln	Gly	Leu	Ile	Gly	Val	Gln	Gln	Pro	Pro		
						725					730						
cag	agt	cag	aac	gtg	ata	aat	aac	caa	caa	gga	act	ccg	gtg	caa	agc	2499	
Gln	Ser	Gln	Asn	Val	Ile	Asn	Asn	Gln	Gln	Gly	Thr	Pro	Val	Gln	Ser		
					740					745					750		
gtg	atg	gtt	tcc	tac	cca	aca	atg	tct	tct	tat	cag	gtg	cca	atg	acc	2547	
Val	Met	Val	Ser	Tyr	Pro	Thr	Met	Ser	Ser	Tyr	Gln	Val	Pro	Met	Thr		
					755					760					765		
cag	ggt	tct	caa	gga	ctg	ccc	cag	cag	tca	tac	caa	cag	cca	atc	atg	2595	
Gln	Gly	Ser	Gln	Gly	Leu	Pro	Gln	Gln	Ser	Tyr	Gln	Gln	Pro	Ile	Met		
				770				775						780			
cta	cct	aac	cag	gca	ggt	caa	ggg	tca	ctc	cca	gcc	act	gga	atg	cct	2643	
Leu	Pro	Asn	Gln	Ala	Gly	Gln	Gly	Ser	Leu	Pro	Ala	Thr	Gly	Met	Pro		
					785			790						795			

16U 100 PCT.ST25
 gtt tac tgt aat gtc aca ccg ccc acc cct cag aac aac ctt agg ctg 2691
 Val Tyr Cys Asn Val Thr Pro Pro Thr Pro Gln Asn Asn Leu Arg Leu
 800 805 810
 att ggc cca cac tgc ccc tcc agc act gtc cca gtg atg tca gct agc 2739
 Ile Gly Pro His Cys Pro Ser Ser Thr Val Pro Val Met Ser Ala Ser
 815 820 825 830
 tgc aga aca aac tgt gca agt atg agc aat gct ggt tgg cag gtc aaa 2787
 Cys Arg Thr Asn Cys Ala Ser Met Ser Asn Ala Gly Trp Gln Val Lys
 835 840 845
 ttc tga gagctctggc tgtggtacat ttcttcagat atttctcatg gcctttgatg 2843
 Phe

gaagaggaac aagggtgggaa aactggctga ggacttaagt attcactcaa cactcaaagt 2903
 attgctgctg gtattctgta aaaaataaac aaagactaat atacacgtta gctggttaat 2963
 ggtgcatatt tctgtcatgt ctgctaggta tgcctttata gcttagctag tgacatgaat 3023
 tcatcaaggt aagattttct cctaccactg aataccactg tgtagattat aatatcccta 3083
 atttggatta gttttgtact ttgtgttgag tttgtgatgc taaaagtatt taaaaattat 3143
 atactaaatc acattgtacc aaagctgtaa tggaaaagca aagaagaatt gatgaattga 3203
 aggaataatt tatatacatt atagagtttt cttttttaat ggatatatac tgtattgtag 3263
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 3369

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Ser Leu Asp Glu Glu Glu Lys Leu Glu Leu Gln Arg Arg Leu Glu Ala
 35 40 45

Gln Asn Gln Glu Arg Arg Lys Ser Lys Ser Gly Ala Gly Lys Gly Lys
 50 55 60

Leu Thr Arg Ser Leu Ala Val Cys Glu Glu Ser Ser Ala Arg Pro Gly
 65 70 75 80

Gly Glu Ser Leu Gln Asp Gln Glu Ser Ile His Leu Gln Leu Ser Ser
 85 90 95

Phe Ser Ser Leu Gln Glu Glu Asp Lys Ser Arg Lys Asp Asp Ser Glu
 100 105 110

Arg Glu Lys Glu Lys Asp Lys Asn Lys Asp Lys Thr Ser Glu Lys Pro
 115 120 125

Lys Ile Arg Met Leu Ser Lys Asp Cys Ser Gln Glu Tyr Thr Asp Ser
 130 135 140

Thr Gly Ile Asp Leu His Glu Phe Leu Ile Asn Thr Leu Lys Asn Asn

16U 100 PCT.ST25

145 150 155 160

Ser Arg Asp Arg Met Ile Leu Leu Lys Met Glu Gln Glu Ile Ile Asp
 165 170 175

Phe Ile Ala Asp Asn Asn Asn His Tyr Lys Lys Phe Pro Gln Met Ser
 180 185 190

Ser Tyr Gln Arg Met Leu Val His Arg Val Ala Ala Tyr Phe Gly Leu
 195 200 205

Asp His Asn Val Asp Gln Thr Gly Lys Ser Val Ile Ile Asn Lys Thr
 210 215 220

Ser Ser Thr Arg Ile Pro Glu Gln Arg Phe Cys Glu His Leu Lys Asp
 225 230 235 240

Glu Lys Gly Glu Glu Ser Gln Lys Arg Phe Ile Leu Lys Arg Asp Asn
 245 250 255

Ser Ser Ile Asp Lys Glu Asp Asn Gln Gln Asn Arg Met His Pro Phe
 260 265 270

Arg Asp Asp Arg Arg Ser Lys Ser Ile Glu Glu Arg Glu Glu Glu Tyr
 275 280 285

Gln Arg Val Arg Glu Arg Ile Phe Ala His Asp Ser Val Cys Ser Gln
 290 295 300

Glu Ser Leu Phe Val Glu Asn Ser Arg Leu Leu Glu Asp Ser Asn Ile
 305 310 315 320

Cys Asn Glu Thr Tyr Lys Lys Arg Gln Leu Phe Arg Gly Asn Arg Asp
 325 330 335

Gly Ser Gly Arg Thr Ser Gly Ser Arg Gln Ser Ser Ser Glu Asn Glu
 340 345 350

Leu Lys Trp Ser Asp His Gln Arg Ala Trp Ser Ser Thr Asp Ser Asp
 355 360 365

Ser Ser Asn Arg Asn Leu Lys Pro Ala Met Thr Lys Thr Ala Ser Phe
 370 375 380

Gly Gly Ile Thr Val Leu Thr Arg Gly Asp Ser Thr Ser Ser Thr Arg
 385 390 395 400

Ser Thr Gly Lys Leu Ser Lys Ala Gly Ser Glu Ser Ser Ser Ser Ala
 405 410 415

Gly Ser Ser Gly Ser Leu Ser Arg Thr His Pro Pro Leu Gln Ser Thr
 420 425 430

Pro Leu Val Ser Gly Val Ala Ala Gly Ser Pro Gly Cys Val Pro Tyr
 435 440 445

Pro Glu Asn Gly Ile Gly Gly Gln Val Ala Pro Ser Ser Thr Ser Tyr
 450 455 460

16U 100 PCT.ST25

Ile Leu Leu Pro Leu Glu Ala Ala Thr Gly Ile Pro Pro Gly Ser Ile
 465 470 475 480

Leu Leu Asn Pro His Thr Gly Gln Pro Phe Val Asn Pro Asp Gly Thr
 485 490 495

Pro Ala Ile Tyr Asn Pro Pro Thr Ser Gln Gln Pro Leu Arg Ser Ala
 500 505 510

Met Val Gly Gln Ser Gln Gln Gln Pro Pro Gln Gln Gln Pro Ser Pro
 515 520 525

Gln Pro Gln Gln Gln Val Gln Pro Pro Gln Pro Gln Met Ala Gly Pro
 530 535 540

Leu Val Thr Gln Ser Val Gln Gly Leu Gln Ala Ser Ser Gln Ser Val
 545 550 555 560

Gln Tyr Pro Ala Val Ser Phe Pro Pro Gln His Leu Leu Pro Val Ser
 565 570 575

Pro Thr Gln His Phe Pro Met Arg Asp Asp Val Ala Thr Gln Phe Gly
 580 585 590

Gln Met Thr Leu Ser Arg Gln Ser Ser Gly Glu Thr Pro Glu Pro Pro
 595 600 605

Ser Gly Pro Val Tyr Pro Ser Ser Leu Met Pro Gln Pro Ala Gln Gln
 610 615 620

Pro Ser Tyr Val Ile Ala Ser Thr Gly Gln Gln Leu Pro Thr Gly Gly
 625 630 635 640

Phe Ser Gly Ser Gly Pro Pro Ile Ser Gln Gln Val Leu Gln Pro Pro
 645 650 655

Pro Ser Pro Gln Gly Phe Val Gln Gln Pro Pro Pro Ala Gln Met Pro
 660 665 670

Val Tyr Tyr Tyr Pro Ser Gly Gln Tyr Pro Thr Ser Thr Thr Gln Gln
 675 680 685

Tyr Arg Pro Met Ala Pro Val Gln Tyr Asn Ala Gln Arg Ser Gln Gln
 690 695 700

Met Pro Gln Ala Ala Gln Gln Ala Gly Tyr Gln Pro Val Leu Ser Gly
 705 710 715 720

Gln Gln Gly Phe Gln Gly Leu Ile Gly Val Gln Gln Pro Pro Gln Ser
 725 730 735

Gln Asn Val Ile Asn Asn Gln Gln Gly Thr Pro Val Gln Ser Val Met
 740 745 750

Val Ser Tyr Pro Thr Met Ser Ser Tyr Gln Val Pro Met Thr Gln Gly
 755 760 765

Ser Gln Gly Leu Pro Gln Gln Ser Tyr Gln Gln Pro Ile Met Leu Pro
 770 775 780

16U 100 PCT.ST25

Asn Gln Ala Gly Gln Gly Ser Leu Pro Ala Thr Gly Met Pro Val Tyr
 785 790 795 800

Cys Asn Val Thr Pro Pro Thr Pro Gln Asn Asn Leu Arg Leu Ile Gly
 805 810 815

Pro His Cys Pro Ser Ser Thr Val Pro Val Met Ser Ala Ser Cys Arg
 820 825 830

Thr Asn Cys Ala Ser Met Ser Asn Ala Gly Trp Gln Val Lys Phe
 835 840 845

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<400> 45
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 tgagggaaga cagagcagtg catggttatg gatactggac aaggatattt ggaaaggttg 120
 acgatgtgtc acactgtgta agggaatcgc atggagatgg gcattccgaa ctgttaatgg 180
 ggacatggga ctccagttgt ctctgatcac ttgtgtggat tttcctggcg tagaacgaca 240
 gaagccgcta gtaagtcgcc aagacctaca gcaggaattc tgcaccaaag ggcataaaat 300
 cttgttattt taatttgcac ctgggaga atg tct gag caa gga gac ctg aat 352
 Met Ser Glu Gln Gly Asp Leu Asn
 1 5
 cag gca ata gca gag gaa gga ggg act gag cag gag acg gcc act cca 400
 Gln Ala Ile Ala Glu Glu Gly Gly Thr Glu Gln Glu Thr Ala Thr Pro
 10 15 20
 gag aac ggc att gtt aaa tca gaa agt ctg gat gaa gag gag aaa ctg 448
 Glu Asn Gly Ile Val Lys Ser Glu Ser Leu Asp Glu Glu Glu Lys Leu
 25 30 35 40
 gaa ctg cag agg cgg ctg gag gct cag aat caa gaa aga aga aaa tcc 496
 Glu Leu Gln Arg Arg Leu Glu Ala Gln Asn Gln Glu Arg Arg Lys Ser
 45 50 55
 aag tca gga gca gga aaa ggt aaa ctg act cgc agt ctt gct gtc tgt 544
 Lys Ser Gly Ala Gly Lys Gly Lys Leu Thr Arg Ser Leu Ala Val Cys
 60 65 70
 gag gaa tct tct gcc aga cca gga ggt gaa agt ctt cag gat cag gaa 592
 Glu Glu Ser Ser Ala Arg Pro Gly Gly Glu Ser Leu Gln Asp Gln Glu
 75 80 85
 tca att cat tta cag ctt tcc agt ttt tcc agc ctg caa gag gag gat 640
 Ser Ile His Leu Gln Leu Ser Ser Phe Ser Ser Leu Gln Glu Glu Asp
 90 95 100
 aaa tct agg aaa gat gac tct gaa aga gaa aaa gaa aag gat aaa aac 688
 Lys Ser Arg Lys Asp Asp Ser Glu Arg Glu Lys Glu Lys Asp Lys Asn
 105 110 115 120
 aaa gat aaa acc tct gaa aaa ccc aag atc aga atg tta tca aaa gat 736
 Lys Asp Lys Thr Ser Glu Lys Pro Lys Ile Arg Met Leu Ser Lys Asp
 125 130 135
 tgc agc caa gaa tac acg gat tct aca ggc ata gac tta cac gag ttt 784
 Cys Ser Gln Glu Tyr Thr Asp Ser Thr Gly Ile Asp Leu His Glu Phe
 140 145 150
 ctg att aac aca tta aag aat aat tcc agg gac agg atg ata ctt ttg 832

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Leu Ile Asn Thr Leu Lys Asn Asn Ser Arg Asp Arg Met Ile Leu Leu	155	160	165	
aaa atg gag cag gaa att att gat ttc att gct gac aac aat aat cat				880
Lys Met Glu Gln Glu Ile Ile Asp Phe Ile Ala Asp Asn Asn Asn His	170	175	180	
tat aaa aag ttc cct cag atg tca tcg tat cag agg atg ctt gtc cat				928
Tyr Lys Lys Phe Pro Gln Met Ser Ser Tyr Gln Arg Met Leu Val His	185	190	195	200
cga gtg gca gct tat ttt gga ttg gat cac aat gtg gat caa aca gga				976
Arg Val Ala Ala Tyr Phe Gly Leu Asp His Asn Val Asp Gln Thr Gly	205	210	215	
aaa tct gtt atc atc aac aag acc agc agc acc aga ata cca gag caa				1024
Lys Ser Val Ile Ile Asn Lys Thr Ser Ser Thr Arg Ile Pro Glu Gln	220	225	230	
agg ttt tgt gaa cat tta aaa gat gaa aaa ggt gaa gaa tcc cag aag				1072
Arg Phe Cys Glu His Leu Lys Asp Glu Lys Gly Glu Ser Gln Lys	235	240	245	
cgg ttt atc ttg aag cga gat aac tct agt att gat aaa gaa gac aat				1120
Arg Phe Ile Leu Lys Arg Asp Asn Ser Ser Ile Asp Lys Glu Asp Asn	250	255	260	
cag caa aac aga atg cat cca ttt aga gat gac aga cga agt aaa tca				1168
Gln Gln Asn Arg Met His Pro Phe Arg Asp Asp Arg Arg Ser Lys Ser	265	270	275	280
att gaa gag aga gaa gag gaa tat cag aga gtg agg gag aga ata ttt				1216
Ile Glu Glu Arg Glu Glu Tyr Gln Arg Val Arg Glu Arg Ile Phe	285	290	295	
gca cac gat tca gtt tgc tcc cag gaa agc ctt ttt gtg gaa aac agg				1264
Ala His Asp Ser Val Cys Ser Gln Glu Ser Leu Phe Val Glu Asn Arg	300	305	310	
ggc aac aga gat ggc tca ggg aga aca tct ggg agt cga cag agc agc				1312
Gly Asn Arg Asp Gly Ser Gly Arg Thr Ser Gly Ser Arg Gln Ser Ser	315	320	325	
tca gaa aat gaa ctc aag tgg tct gac cac caa agg gcc tgg agc agc				1360
Ser Glu Asn Glu Leu Lys Trp Ser Asp His Gln Arg Ala Trp Ser Ser	330	335	340	
aca gac tcc gac agt tcc aac cgc aat cta aag ccc gcc atg acc aag				1408
Thr Asp Ser Asp Ser Ser Asn Arg Asn Leu Lys Pro Ala Met Thr Lys	345	350	355	360
acg gcg agt ttt ggg ggc atc acg gtg ctg acc agg ggt gac agc act				1456
Thr Ala Ser Phe Gly Gly Ile Thr Val Leu Thr Arg Gly Asp Ser Thr	365	370	375	
tcc agt act agg agt acc ggg aag ctg tcc aaa gca ggt tcc gag tct				1504
Ser Ser Thr Arg Ser Thr Gly Lys Leu Ser Lys Ala Gly Ser Glu Ser	380	385	390	
tcc agc agt gca ggc tcc tca gga tcg ctg tcc cgc acc cat cca cct				1552
Ser Ser Ser Ala Gly Ser Ser Gly Ser Leu Ser Arg Thr His Pro Pro	395	400	405	
ctc cag agc aca ccc cta gtc tca ggt gtg gca gct ggc tct cca ggc				1600
Leu Gln Ser Thr Pro Leu Val Ser Gly Val Ala Ala Gly Ser Pro Gly	410	415	420	
tgt gtg cct tat cca gag aat gga ata ggg ggc cag gtt gct ccc agc				1648
Cys Val Pro Tyr Pro Glu Asn Gly Ile Gly Gln Val Ala Pro Ser	425	430	435	440
agc acc agc tac atc ctc ctt cca ctt gaa gct gca aca ggc atc ccg				1696
Ser Thr Ser Tyr Ile Leu Leu Pro Leu Glu Ala Ala Thr Gly Ile Pro	445	450	455	
cct gga agc atc ctt ctt aat cca cac aca ggc cag ccc ttt gtg aat				1744
Pro Gly Ser Ile Leu Leu Asn Pro His Thr Gly Gln Pro Phe Val Asn	460	465	470	

16U 100 PCT.ST25																
ccc gat gga act cct gca ata tac aac cca ccc acc agt cag cag ccc	Pro Asp Gly Thr Pro Ala Ile Tyr Asn Pro Pro Thr Ser Gln Gln Pro	475	480	485												1792
ctg cga agc gcc atg gtg ggg cag tcc caa cag cag ccg cca cag cag	Leu Arg Ser Ala Met Val Gly Gln Ser Gln Gln Gln Pro Pro Gln Gln	490	495	500												1840
cag ccc tcc ccg cag ccc caa cag cag gtc cag cca ccg cag cca cag	Gln Pro Ser Pro Gln Pro Gln Gln Gln Val Gln Pro Pro Gln Pro Gln	505	510	515												1888
atg gca ggc cct ctg gtc act cag tct gtc cag ggg ctg cag gct tcc	Met Ala Gly Pro Leu Val Thr Gln Ser Val Gln Gly Leu Gln Ala Ser	525	530	535												1936
tcc cag tca gtg caa tat ccg gca gtc tct ttt cct ccc cag cac ctc	Ser Gln Ser Val Gln Tyr Pro Ala Val Ser Phe Pro Pro Gln His Leu	540	545	550												1984
cta cct gtg tct cca acg cag cac ttt ccc atg aga gat gat gtg gca	Leu Pro Val Ser Pro Thr Gln His Phe Pro Met Arg Asp Asp Val Ala	555	560	565												2032
aca cag ttt ggc cag atg acc ctg agc cgg cag tcc tcg ggg gag act	Thr Gln Phe Gly Gln Met Thr Leu Ser Arg Gln Ser Ser Ser Gly Glu Thr	570	575	580												2080
cct gaa ccc cca tca ggt cct gtc tac cca tcc tcc ctt atg cca cag	Pro Glu Pro Pro Ser Gly Pro Val Tyr Pro Ser Ser Leu Met Pro Gln	585	590	595												2128
ccg gcc cag cag ccc agc tat gta atc gcc tct aca ggc cag cag ctt	Pro Ala Gln Gln Pro Ser Tyr Val Ile Ala Ser Thr Gly Gln Gln Leu	605	610	615												2176
cct aca gga gga ttc tca ggc tct ggc cct ccc atc tcc cag cag gtc	Pro Thr Gly Gly Phe Ser Gly Ser Gly Pro Pro Ile Ser Gln Gln Val	620	625	630												2224
ctc cag ccc cct ccc tca cca cag gga ttt gtg caa cag cct ccg cct	Leu Gln Pro Pro Pro Ser Pro Gln Gly Phe Val Gln Gln Pro Pro Pro	635	640	645												2272
gca cag atg cct gta tat tat tac cca tct ggt cag tac cct acc tca	Ala Gln Met Pro Val Tyr Tyr Tyr Pro Ser Gly Gln Tyr Pro Thr Ser	650	655	660												2320
acc acg caa cag tac ccg ccc atg gcc ccg gtt cag tac aac gct cag	Thr Thr Gln Gln Tyr Arg Pro Met Ala Pro Val Gln Tyr Asn Ala Gln	665	670	675												2368
agg agt caa cag atg cca cag gca gca cag caa gca ggt tac cag cca	Arg Ser Gln Gln Met Pro Gln Ala Ala Gln Gln Ala Gly Tyr Gln Pro	685	690	695												2416
gtc ttg tct ggt caa cag gga ttc caa ggc cta ata gga gtg cag cag	Val Leu Ser Gly Gln Gln Gly Phe Gln Gly Leu Ile Gly Val Gln Gln	700	705	710												2464
cca cct cag agt cag aac gtg ata aat aac caa caa gga act ccg gtg	Pro Pro Gln Ser Gln Asn Val Ile Asn Asn Gln Gln Gly Thr Pro Val	715	720	725												2512
caa agc gtg atg gtt tcc tac cca aca atg tct tct tat cag gtg cca	Gln Ser Val Met Val Ser Tyr Pro Thr Met Ser Ser Tyr Gln Val Pro	730	735	740												2560
atg acc cag ggt tct caa gga ctg ccc cag cag tca tac caa cag cca	Met Thr Gln Gly Ser Gln Gly Leu Pro Gln Gln Ser Tyr Gln Gln Pro	745	750	755												2608
atc atg cta cct aac cag gca ggt caa ggg tca ctc cca gcc act gga	Ile Met Leu Pro Asn Gln Ala Gly Gln Gly Ser Leu Pro Ala Thr Gly	765	770	775												2656
atg cct gtt tac tgt aat gtc aca ccg ccc acc cct cag aac aac ctt	Met Pro Val Tyr Cys Asn Val Thr Pro Pro Thr Pro Gln Asn Asn Leu	780	785	790												2704

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agg ctg att ggc cca cac tgc ccc tcc agc act gtc cca gtg atg tca 2752
 Arg Leu Ile Gly Pro His Cys Pro Ser Ser Thr Val Pro Val Met Ser
 795 800 805

gct agc tgc aga aca aac tgt gca agt atg agc aat gct ggt tgg cag 2800
 Ala Ser Cys Arg Thr Asn Cys Ala Ser Met Ser Asn Ala Gly Trp Gln
 810 815 820

gtc aaa ttc tga gagctctggc tgtggtacat ttcttcagat atttctcatg 2852
 Val Lys Phe
 825

gcctttgatg gaagaggaac aaggtgggaa aactggctga ggacttaagt attcactcaa 2912
 cactcaaattg attgctgctg gtattctgta aaaaataaac aaagactaat atacacgtta 2972
 gctgggttaat ggtgcatatt tctgtcatgt ctgctaggtg tgcctttata gcttagctag 3032
 tgacatgaat tcatcaaggt aagattttct cctaccactg aataccactg tgtagattat 3092
 aatatcccta atttggatta gttttgtact ttgtgttgag tttgtgatgc taaaagtatt 3152
 taaaaattat atactaaatc acattgtacc aaagctgtaa tggaaaagca aagaagaatt 3212
 gatgaattga aggaataatt tatatacatt atagagtttt cttttttaat ggatatatac 3272
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 taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 3374

<210> 46
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<400> 46

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 20 25 30

Ser Leu Asp Glu Glu Glu Lys Leu Glu Leu Gln Arg Arg Leu Glu Ala
 35 40 45

Gln Asn Gln Glu Arg Arg Lys Ser Lys Ser Gly Ala Gly Lys Gly Lys
 50 55 60

Leu Thr Arg Ser Leu Ala Val Cys Glu Glu Ser Ser Ala Arg Pro Gly
 65 70 75 80

Gly Glu Ser Leu Gln Asp Gln Glu Ser Ile His Leu Gln Leu Ser Ser
 85 90 95

Phe Ser Ser Leu Gln Glu Glu Asp Lys Ser Arg Lys Asp Asp Ser Glu
 100 105 110

Arg Glu Lys Glu Lys Asp Lys Asn Lys Asp Lys Thr Ser Glu Lys Pro
 115 120 125

Lys Ile Arg Met Leu Ser Lys Asp Cys Ser Gln Glu Tyr Thr Asp Ser
 130 135 140

Thr Gly Ile Asp Leu His Glu Phe Leu Ile Asn Thr Leu Lys Asn Asn
 145 150 155 160

160 100 PCT.ST25

Ser Arg Asp Arg Met Ile Leu Leu Lys Met Glu Gln Glu Ile Ile Asp
165 170 175

Phe Ile Ala Asp Asn Asn Asn His Tyr Lys Lys Phe Pro Gln Met Ser
180 185 190

Ser Tyr Gln Arg Met Leu Val His Arg Val Ala Ala Tyr Phe Gly Leu
195 200 205

Asp His Asn Val Asp Gln Thr Gly Lys Ser Val Ile Ile Asn Lys Thr
210 215 220

Ser Ser Thr Arg Ile Pro Glu Gln Arg Phe Cys Glu His Leu Lys Asp
225 230 235 240

Glu Lys Gly Glu Glu Ser Gln Lys Arg Phe Ile Leu Lys Arg Asp Asn
245 250 255

Ser Ser Ile Asp Lys Glu Asp Asn Gln Gln Asn Arg Met His Pro Phe
260 265 270

Arg Asp Asp Arg Arg Ser Lys Ser Ile Glu Glu Arg Glu Glu Glu Tyr
275 280 285

Gln Arg Val Arg Glu Arg Ile Phe Ala His Asp Ser Val Cys Ser Gln
290 295 300

Glu Ser Leu Phe Val Glu Asn Arg Gly Asn Arg Asp Gly Ser Gly Arg
305 310 315 320

Thr Ser Gly Ser Arg Gln Ser Ser Ser Glu Asn Glu Leu Lys Trp Ser
325 330 335

Asp His Gln Arg Ala Trp Ser Ser Thr Asp Ser Asp Ser Ser Asn Arg
340 345 350

Asn Leu Lys Pro Ala Met Thr Lys Thr Ala Ser Phe Gly Gly Ile Thr
355 360 365

Val Leu Thr Arg Gly Asp Ser Thr Ser Ser Thr Arg Ser Thr Gly Lys
370 375 380

Leu Ser Lys Ala Gly Ser Glu Ser Ser Ser Ser Ala Gly Ser Ser Gly
385 390 395 400

Ser Leu Ser Arg Thr His Pro Pro Leu Gln Ser Thr Pro Leu Val Ser
405 410 415

Gly Val Ala Ala Gly Ser Pro Gly Cys Val Pro Tyr Pro Glu Asn Gly
420 425 430

Ile Gly Gly Gln Val Ala Pro Ser Ser Thr Ser Tyr Ile Leu Leu Pro
435 440 445

Leu Glu Ala Ala Thr Gly Ile Pro Pro Gly Ser Ile Leu Leu Asn Pro
450 455 460

His Thr Gly Gln Pro Phe Val Asn Pro Asp Gly Thr Pro Ala Ile Tyr
465 470 475 480

16U 100 PCT.ST25

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Tyr Pro Ser Ser Leu Met Pro Gln Pro Ala Gln Gln Pro Ser Tyr Val
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16U 100 PCT.ST25

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Glu Leu Gln Arg Arg Leu Glu Ala Gln Asn Gln Glu Arg Arg Lys Ser
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Lys Ser Gly Ala Gly Lys Gly Lys Leu Thr Arg Ser Leu Ala Val Cys
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Ser Ile His Leu Gln Leu Ser Ser Phe Ser Ser Leu Gln Glu Glu Asp
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Lys Asp Lys Thr Ser Glu Lys Pro Lys Ile Arg Met Leu Ser Lys Asp
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Leu Ile Asn Thr Leu Lys Asn Asn Ser Arg Asp Arg Met Ile Leu Leu
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170 175 180

160 100 PCT.ST25

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16U 100 PCT.ST25

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16U 100 PCT.ST25

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tcc ccg cag ccc caa cag cag gtc cag cca ccg cag cca cag atg gca Ser Pro Gln Pro Gln Gln Gln Val Gln Pro Pro Gln Pro Gln Met Ala 475 480 485	1792
ggc cct ctg gtc act cag tct gtc cag ggg ctg cag gct tcc tcc cag Gly Pro Leu Val Thr Gln Ser Val Gln Gly Leu Gln Ala Ser Ser Gln 490 495 500	1840
tca gtg caa tat ccg gca gtc tct ttt cct ccc cag cac ctc cta cct Ser Val Gln Tyr Pro Ala Val Ser Phe Pro Pro Gln His Leu Leu Pro 505 510 515 520	1888
gtg tct cca acg cag cac ttt ccc atg aga gat gat gtg gca aca cag Val Ser Pro Thr Gln His Phe Pro Met Arg Asp Asp Val Ala Thr Gln 525 530 535	1936
ttt ggc cag atg acc ctg agc cgg cag tcc tgc ggg gag act cct gaa Phe Gly Gln Met Thr Leu Ser Arg Gln Ser Ser Gly Glu Thr Pro Glu 540 545 550	1984
ccc cca tca ggt cct gtc tac cca tcc tcc ctt atg cca cag ccg gcc Pro Pro Ser Gly Pro Val Tyr Pro Ser Ser Leu Met Pro Gln Pro Ala	2032

16U 100 PCT.ST25
565

555 560

cag cag ccc agc tat gta atc gcc tct aca ggc cag cag ctt cct aca 2080
Gln Gln Pro Ser Tyr Val Ile Ala Ser Thr Gly Gln Gln Leu Pro Thr
570 575 580

gga gga ttc tca ggc tct ggc cct ccc atc tcc cag cag gtc ctc cag 2128
Gly Gly Phe Ser Gly Ser Gly Pro Pro Ile Ser Gln Gln Val Leu Gln
585 590 595 600

ccc cct ccc tca cca cag gga tty gtg caa cag cct ccg cct gca cag 2176
Pro Pro Pro Ser Pro Gln Gly Phe Val Gln Gln Pro Pro Pro Ala Gln
605 610 615

atg cct gta tat tat tac cca tct ggt cag tac cct acc tca acc acg 2224
Met Pro Val Tyr Tyr Pro Ser Gly Gln Tyr Pro Thr Ser Thr Thr
620 625 630

caa cag tac cgg ccc atg gcc ccg gtt cag tac aac gct cag agg agt 2272
Gln Gln Tyr Arg Pro Met Ala Pro Val Gln Tyr Asn Ala Gln Arg Ser
635 640 645

caa cag atg cca cag gca gca cag caa gca ggt tac cag cca gtc ttg 2320
Gln Gln Met Pro Gln Ala Ala Gln Gln Ala Gly Tyr Gln Pro Val Leu
650 655 660

tct ggt caa cag gga ttc cca ggc cta ata gga gtg cag cag cca cct 2368
Ser Gly Gln Gln Gly Phe Gln Gly Leu Ile Gly Val Gln Gln Pro Pro
665 670 675 680

cag agt cag aac gtg ata aat aac caa caa gga act ccg gtg caa agc 2416
Gln Ser Gln Asn Val Ile Asn Asn Gln Gln Gly Thr Pro Val Gln Ser
685 690 695

gtg atg gtt tcc tac cca aca atg tct tct tat cag gtg cca atg acc 2464
Val Met Val Ser Tyr Pro Thr Met Ser Ser Tyr Gln Val Pro Met Thr
700 705 710

cag ggt tct caa gga ctg ccc cag cag tca tac caa cag cca atc atg 2512
Gln Gly Ser Gln Gly Leu Pro Gln Gln Ser Tyr Gln Gln Pro Ile Met
715 720 725

cta cct aac cag gca ggt caa ggg tca ctc cca gcc act gga atg cct 2560
Leu Pro Asn Gln Ala Gly Gln Gly Ser Leu Pro Ala Thr Gly Met Pro
730 735 740

gtt tac tgt aat gtc aca ccg ccc acc cct cag aac aac ctt agg ctg 2608
Val Tyr Cys Asn Val Thr Pro Pro Thr Pro Gln Asn Asn Leu Arg Leu
745 750 755 760

att ggc cca cac tgc ccc tcc agc act gtc cca gtg atg tca gct agc 2656
Ile Gly Pro His Cys Pro Ser Ser Thr Val Pro Val Met Ser Ala Ser
765 770 775

tgc aga aca aac tgt gca agt atg agc aat gct ggt tgg cag gtc aaa 2704
Cys Arg Thr Asn Cys Ala Ser Met Ser Asn Ala Gly Trp Gln Val Lys
780 785 790

ttc tga gagctctggc tgtggtacat ttcttcagat atttctcatg gcctttgatg 2760
Phe

gaagaggaac aaggtgggaa aactggctga ggacttaagt attcactcaa cactcaaatg 2820

attgctgctg gtattctgta aaaartaaac aaagactaat atacacgtta gctgggtaat 2880

ggtgcatatt tctgtcatgt ctgctaggta tgcctttata gcttagctag tgacatgaat 2940

tcatacagggt aagattytct cctaccactg aataccactg tgtagattat aatatcccta 3000

atttggatta gttttgtact ttgtgttgag tttgtgatgc taaaagtatt taaaaattat 3060

atactaaatc acattgtacc aaagctgtaa tggaaaagca aagaagaayt gatgaattga 3120

aggaataatt tatatacatt atagagtttt cttttttaat ggatatatac tgtattgtag 3180

tgtttaataca aaataaaact atttgacctt atggaggaag gtcatgtttt taaaaaaaaa 3240

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 3272

16U 100 PCT.ST25

<210> 50
 <211> 793
 <212> PRT
 <213> Homo sapiens

<400> 50

Met Ser Glu Gln Gly Asp Leu Asn Gln Ala Ile Ala Glu Glu Gly Gly
 1 5 10 15

Thr Glu Gln Glu Thr Ala Thr Pro Glu Asn Gly Ile Val Lys Ser Glu
 20 25 30

Ser Leu Asp Glu Glu Glu Lys Leu Glu Leu Gln Arg Arg Leu Glu Ala
 35 40 45

Gln Asn Gln Glu Arg Arg Lys Ser Lys Ser Gly Ala Gly Lys Gly Lys
 50 55 60

Leu Thr Arg Ser Leu Ala Val Cys Glu Glu Ser Ser Ala Arg Pro Gly
 65 70 75 80

Gly Glu Ser Leu Gln Asp Gln Glu Ser Ile His Leu Gln Leu Ser Ser
 85 90 95

Phe Ser Ser Leu Gln Glu Glu Asp Lys Ser Arg Lys Asp Asp Ser Glu
 100 105 110

Arg Glu Lys Glu Lys Asp Lys Asn Lys Asp Lys Thr Ser Glu Lys Pro
 115 120 125

Lys Ile Arg Met Leu Ser Lys Asp Cys Ser Gln Glu Tyr Thr Asp Ser
 130 135 140

Thr Gly Ile Asp Leu His Glu Phe Leu Ile Asn Thr Leu Lys Asn Asn
 145 150 155 160

Ser Arg Asp Arg Met Ile Leu Leu Lys Met Glu Gln Glu Ile Ile Asp
 165 170 175

Phe Ile Ala Asp Asn Asn Asn His Tyr Lys Lys Phe Pro Gln Met Ser
 180 185 190

Ser Tyr Gln Arg Met Leu Val His Arg Val Ala Ala Tyr Phe Gly Leu
 195 200 205

Asp His Asn Val Asp Gln Thr Gly Lys Ser Val Ile Ile Asn Lys Thr
 210 215 220

Ser Ser Thr Arg Ile Pro Glu Gln Arg Phe Cys Glu His Leu Lys Asp
 225 230 235 240

Glu Lys Gly Glu Glu Ser Gln Lys Arg Phe Ile Leu Lys Arg Asp Asn
 245 250 255

Ser Ser Ile Asp Lys Glu Asp Asn Gln Ser Val Cys Ser Gln Glu Ser
 260 265 270

Leu Phe Val Glu Asn Arg Gly Asn Arg Asp Gly Ser Gly Arg Thr Ser
 275 280 285

16U 100 PCT.ST25

Gly Ser Arg Gln Ser Ser Ser Glu Asn Glu Leu Lys Trp Ser Asp His
 290 295 300

Gln Arg Ala Trp Ser Ser Thr Asp Ser Asp Ser Ser Asn Arg Asn Leu
 305 310 315 320

Lys Pro Ala Met Thr Lys Thr Ala Ser Phe Gly Gly Ile Thr Val Leu
 325 330 335

Thr Arg Gly Asp Ser Thr Ser Ser Thr Arg Ser Thr Gly Lys Leu Ser
 340 345 350

Lys Ala Gly Ser Glu Ser Ser Ser Ser Ala Gly Ser Ser Gly Ser Leu
 355 360 365

Ser Arg Thr His Pro Pro Leu Gln Ser Thr Pro Leu Val Ser Gly Val
 370 375 380

Ala Ala Gly Ser Pro Gly Cys Val Pro Tyr Pro Glu Asn Gly Ile Gly
 385 390 395 400

Gly Gln Val Ala Pro Ser Ser Thr Ser Tyr Ile Leu Leu Pro Leu Glu
 405 410 415

Ala Ala Thr Gly Ile Pro Pro Gly Ser Ile Leu Leu Asn Pro His Thr
 420 425 430

Gly Gln Pro Phe Val Asn Pro Asp Gly Thr Pro Ala Ile Tyr Asn Pro
 435 440 445

Pro Thr Ser Gln Gln Pro Leu Arg Ser Ala Met Val Gly Gln Ser Gln
 450 455 460

Gln Gln Pro Pro Gln Gln Gln Pro Ser Pro Gln Pro Gln Gln Val
 465 470 475 480

Gln Pro Pro Gln Pro Gln Met Ala Gly Pro Leu Val Thr Gln Ser Val
 485 490 495

Gln Gly Leu Gln Ala Ser Ser Gln Ser Val Gln Tyr Pro Ala Val Ser
 500 505 510

Phe Pro Pro Gln His Leu Leu Pro Val Ser Pro Thr Gln His Phe Pro
 515 520 525

Met Arg Asp Asp Val Ala Thr Gln Phe Gly Gln Met Thr Leu Ser Arg
 530 535 540

Gln Ser Ser Gly Glu Thr Pro Glu Pro Pro Ser Gly Pro Val Tyr Pro
 545 550 555 560

Ser Ser Leu Met Pro Gln Pro Ala Gln Gln Pro Ser Tyr Val Ile Ala
 565 570 575

Ser Thr Gly Gln Gln Leu Pro Thr Gly Gly Phe Ser Gly Ser Gly Pro
 580 585 590

Pro Ile Ser Gln Gln Val Leu Gln Pro Pro Pro Ser Pro Gln Gly Phe

16U 100 PCT.ST25
605

595 600

Val Gln Gln Pro Pro Pro Ala Gln Met Pro Val Tyr Tyr Tyr Pro Ser
610 615 620

Gly Gln Tyr Pro Thr Ser Thr Thr Gln Gln Tyr Arg Pro Met Ala Pro
625 630 635 640

Val Gln Tyr Asn Ala Gln Arg Ser Gln Gln Met Pro Gln Ala Ala Gln
645 650 655

Gln Ala Gly Tyr Gln Pro Val Leu Ser Gly Gln Gln Gly Phe Gln Gly
660 665 670

Leu Ile Gly Val Gln Gln Pro Pro Gln Ser Gln Asn Val Ile Asn Asn
675 680 685

Gln Gln Gly Thr Pro Val Gln Ser Val Met Val Ser Tyr Pro Thr Met
690 695 700

Ser Ser Tyr Gln Val Pro Met Thr Gln Gly Ser Gln Gly Leu Pro Gln
705 710 715 720

Gln Ser Tyr Gln Gln Pro Ile Met Leu Pro Asn Gln Ala Gly Gln Gly
725 730 735

Ser Leu Pro Ala Thr Gly Met Pro Val Tyr Cys Asn Val Thr Pro Pro
740 745 750

Thr Pro Gln Asn Asn Leu Arg Leu Ile Gly Pro His Cys Pro Ser Ser
755 760 765

Thr Val Pro Val Met Ser Ala Ser Cys Arg Thr Asn Cys Ala Ser Met
770 775 780

Ser Asn Ala Gly Trp Gln Val Lys Phe
785 790

<210> 51
<211> 1006
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (280)..(549)
<223>

<400> 51
gggcagcttg agacaggtgg agctggatca agctgtgaac gtgatttgct ggaagctggt 60
cattagtgtt gacgatgtgt cacactgtgt aagggaatcg catggagatg ggcattccga 120
actgttaatg gggacatggg actccagttg tctctgatca cttgtgtgga ttttcctggc 180
gtagaacgac agaagccgct agtaagtcgc caagacctac agcaggaatt ctgcaccaaa 240
gggcataaaa tcttgttatt ttaatttgca tctgggaga atg tct gag caa gga 294
Met Ser Glu Gln Gly
1 5
gac ctg aat cag gca ata gca gag gaa gga ggg act gag cag gag acg 342
Asp Leu Asn Gln Ala Ile Ala Glu Glu Gly Gly Thr Glu Gln Glu Thr 20
10 15 20
gcc act cca gag aac ggc att gtt aaa tca gaa agt ctg gat gaa gag 390

16U 100 PCT.ST25

Ala Thr Pro	Glu Asn Gly Ile Val Lys Ser	Glu Ser Leu Asp Glu Glu	
	25	30	35
gag aaa ctg gaa ctg cag agg cgg ctg gag gct cag aat caa gaa aga			438
Glu Lys Leu Glu Leu Gln Arg Arg Leu Glu Ala Gln Asn Gln Glu Arg			
	40	45	50
aga aaa tcc aag tca gga gca gga aaa ggt aaa ctg act cgc agt ctt			486
Arg Lys Ser Lys Ser Gly Ala Gly Lys Gly Lys Leu Thr Arg Ser Leu			
	55	60	65
gct gtc tgt gag gaa tct tct gcc aga cca gga ggt gaa agt ctt cag			534
Ala Val Cys Glu Glu Ser Ser Ala Arg Pro Gly Gly Glu Ser Leu Gln			
	70	75	80
gat cag act ctc tga aaactgcaaa tggaaaggaa ttcaaaagaa tttagattaa			589
Asp Gln Thr Leu			
aagttaaata aaaagtaggc acagtagtgc tgaattttcc tcaaaggctc tcttttgata			649
aggctgaacc aaatataatc ccaagtatcc tctctccttc cttgttgag atgtcttacc			709
tctcagctcc caaaatgcac ttgcctataa gaaacacaat tgctggttca tatgaaactt			769
wagaaatagt gaataagggt catttaactt tggagaaata cttttatgsc tttggtggag			829
atttctcaat actgcaaaag ttgtccagaa atgaatctga gctgatggtg actttaagtt			889
aatattatta atatatcact gcatattttt acccttattt ttgctcctta cagcaagatt			949
agtaggttat aaaaatttaa atttaaacaa aattatttca tgacaaaatg ggaaact			1006

<210> 52
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 52

Met Ser Glu Gln Gly Asp Leu Asn Gln Ala Ile Ala Glu Glu Gly Gly
 1 5 10 15

Thr Glu Gln Glu Thr Ala Thr Pro Glu Asn Gly Ile Val Lys Ser Glu
 20 25 30

Ser Leu Asp Glu Glu Glu Lys Leu Glu Leu Gln Arg Arg Leu Glu Ala
 35 40 45

Gln Asn Gln Glu Arg Arg Lys Ser Lys Ser Gly Ala Gly Lys Gly Lys
 50 55 60

Leu Thr Arg Ser Leu Ala Val Cys Glu Glu Ser Ser Ala Arg Pro Gly
 65 70 75 80

Gly Glu Ser Leu Gln Asp Gln Thr Leu
 85

<210> 53
 <211> 807
 <212> PRT
 <213> Mus musculus

<400> 53

Met Ser Glu Gln Gly Gly Leu Thr Pro Thr Ile Leu Glu Glu Gly Gln
 1 5 10 15

Thr Glu Pro Glu Ser Ala Pro Glu Asn Gly Ile Leu Lys Ser Glu Ser
 20 25 30

16U 100 PCT.ST25

Leu Asp Glu Glu Glu Lys Leu Glu Leu Gln Arg Arg Leu Ala Ala Gln
 35 40 45

Asn Gln Glu Arg Arg Lys Ser Lys Ser Gly Ala Gly Lys Gly Lys Leu
 50 55 60

Thr Arg Ser Leu Ala Val Cys Glu Glu Ser Ser Ala Arg Ser Gly Gly
 65 70 75 80

Glu Ser His Gln Asp Gln Glu Ser Ile His Leu Gln Leu Ser Ser Phe
 85 90 95

Pro Ser Leu Gln Glu Glu Asp Lys Ser Arg Lys Asp Asp Ser Glu Arg
 100 105 110

Glu Lys Glu Lys Asp Lys Asn Arg Glu Lys Leu Ser Glu Arg Pro Lys
 115 120 125

Ile Arg Met Leu Ser Lys Asp Cys Ser Gln Glu Tyr Thr Asp Ser Thr
 130 135 140

Gly Ile Asp Leu His Gly Phe Leu Ile Asn Thr Leu Lys Asn Asn Ser
 145 150 155 160

Arg Asp Arg Met Ile Leu Leu Lys Met Glu Gln Glu Met Ile Asp Phe
 165 170 175

Ile Ala Asp Ser Asn Asn His Tyr Lys Lys Phe Pro Gln Met Ser Ser
 180 185 190

Tyr Gln Arg Met Leu Val His Arg Val Ala Ala Tyr Phe Gly Leu Asp
 195 200 205

His Asn Val Asp Gln Thr Gly Lys Ser Val Ile Ile Asn Lys Thr Ser
 210 215 220

Ser Thr Arg Ile Pro Glu Gln Arg Phe Cys Glu His Leu Lys Asp Glu
 225 230 235 240

Lys Ser Glu Glu Ser Gln Lys Arg Phe Ile Leu Lys Arg Asp Asn Ser
 245 250 255

Ser Ile Asp Lys Glu Asp Asn Gln Asn Arg Met His Pro Phe Arg Asp
 260 265 270

Asp Arg Arg Ser Lys Ser Ile Glu Glu Arg Glu Glu Glu Tyr Gln Arg
 275 280 285

Val Arg Glu Arg Ile Phe Ala His Asp Ser Val Cys Ser Gln Glu Ser
 290 295 300

Leu Phe Leu Asp Asn Ser Arg Leu Gln Glu Asp Met His Ile Cys Asn
 305 310 315 320

Glu Thr Tyr Lys Lys Arg Gln Leu Phe Arg Ala His Arg Asp Ser Ser
 325 330 335

Gly Arg Thr Ser Gly Ser Arg Gln Ser Ser Ser Glu Thr Glu Leu Arg
 340 345 350

16U 100 PCT.ST25

Trp Pro Asp His Gln Arg Ala Trp Ser Ser Thr Asp Ser Asp Ser Ser
 355 360 365

Asn Arg Asn Leu Lys Pro Thr Met Thr Lys Thr Ala Ser Phe Gly Gly
 370 375 380

Ile Thr Val Leu Thr Arg Gly Asp Ser Thr Ser Ser Thr Arg Ser Ala
 385 390 395 400

Gly Lys Leu Ser Lys Thr Gly Ser Glu Ser Ser Ser Ser Ala Gly Ser
 405 410 415

Ser Gly Ser Leu Ser Arg Thr His Pro Gln Ser Thr Ala Leu Thr Ser
 420 425 430

Ser Val Ala Ala Gly Ser Pro Gly Cys Met Ala Tyr Ser Glu Asn Gly
 435 440 445

Met Gly Gly Gln Val Pro Pro Ser Ser Thr Ser Tyr Ile Leu Leu Pro
 450 455 460

Leu Glu Ser Ala Thr Gly Ile Pro Pro Gly Ser Ile Leu Leu Asn Pro
 465 470 475 480

His Thr Gly Gln Pro Phe Val Asn Pro Asp Gly Thr Pro Ala Ile Tyr
 485 490 495

Asn Pro Pro Gly Ser Gln Gln Thr Leu Arg Gly Thr Val Gly Gly Gln
 500 505 510

Pro Gln Gln Pro Pro Gln Gln Gln Pro Ser Pro Gln Pro Gln Gln Gln
 515 520 525

Val Gln Ala Ser Gln Pro Gln Met Ala Gly Pro Leu Val Thr Gln Arg
 530 535 540

Glu Glu Leu Ala Ala Gln Phe Ser Gln Leu Ser Met Ser Arg Gln Ser
 545 550 555 560

Ser Gly Asp Thr Pro Glu Pro Pro Ser Gly Thr Val Tyr Pro Ala Ser
 565 570 575

Leu Leu Pro Gln Thr Ala Gln Pro Gln Ser Tyr Val Ile Thr Ser Ala
 580 585 590

Gly Gln Gln Leu Ser Thr Gly Gly Phe Ser Asp Ser Gly Pro Pro Ile
 595 600 605

Ser Gln Gln Val Leu Gln Ala Pro Pro Ser Pro Gln Gly Phe Val Gln
 610 615 620

Gln Pro Pro Pro Ala Gln Met Ser Val Tyr Tyr Tyr Pro Ser Gly Gln
 625 630 635 640

Tyr Pro Thr Ser Thr Ser Gln Gln Tyr Arg Pro Leu Ala Ser Val Gln
 645 650 655

Tyr Ser Ala Gln Arg Ser Gln Gln Ile Pro Gln Thr Thr Gln Gln Ala

16U 100 PCT.ST25
660 665 670

Gly Tyr Gln Pro Val Leu Ser Gly Gln Gln Gly Phe Gln Gly Met Met
675 680 685

Gly Val Gln Gln Ser Ala His Ser Gln Gly Val Met Ser Ser Gln Gln
690 695 700

Gly Ala Pro Val His Gly Val Met Val Ser Tyr Pro Thr Met Ser Ser
705 710 715 720

Tyr Gln Val Pro Met Thr Gln Gly Ser Gln Ala Val Pro Gln Gln Thr
725 730 735

Tyr Gln Pro Pro Ile Met Leu Pro Ser Gln Ala Gly Gln Gly Ser Leu
740 745 750

Pro Ala Thr Gly Met Pro Val Tyr Cys Asn Val Thr Pro Pro Asn Pro
755 760 765

Gln Asn Asn Leu Arg Leu Met Gly Pro His Cys Pro Ser Ser Thr Val
770 775 780

Pro Val Met Ser Ala Ser Cys Arg Thr Asn Cys Gly Asn Val Ser Asn
785 790 795 800

Ala Gly Trp Gln Val Lys Phe
805

<210> 54
<211> 648
<212> PRT
<213> Homo sapien

<400> 54

Met Ile Leu Leu Lys Met Glu Gln Glu Ile Ile Asp Phe Ile Ala Asp
1 5 10 15

Asn Asn Asn His Tyr Lys Lys Phe Pro Gln Met Ser Ser Tyr Gln Arg
20 25 30

Met Leu Val His Arg Val Ala Ala Tyr Phe Gly Leu Asp His Asn Val
35 40 45

Asp Gln Thr Gly Lys Ser Val Ile Ile Asn Lys Thr Ser Ser Thr Arg
50 55 60

Ile Pro Glu Gln Arg Phe Cys Glu His Leu Lys Asp Glu Lys Gly Glu
65 70 75 80

Glu Ser Gln Lys Arg Phe Ile Leu Lys Arg Asp Asn Ser Ser Ile Asp
85 90 95

Lys Glu Asp Asn Gln Ser Val Cys Ser Gln Glu Ser Leu Phe Val Glu
100 105 110

Asn Arg Leu Leu Glu Asp Ser Asn Ile Cys Asn Glu Thr Tyr Lys Lys
115 120 125

Arg Gln Leu Phe Arg Gly Asn Arg Asp Gly Ser Gly Arg Thr Ser Gly

130 135 16U 100 PCT.ST25
140

Ser Arg Gln Ser Ser Ser Glu Asn Glu Leu Lys Trp Ser Asp His Gln
145 150 155 160

Arg Ala Trp Ser Ser Thr Asp Ser Asp Ser Ser Asn Arg Asn Leu Lys
165 170 175

Pro Ala Met Thr Lys Thr Ala Ser Phe Gly Gly Ile Thr Val Leu Thr
180 185 190

Arg Gly Asp Ser Thr Ser Ser Thr Arg Ser Thr Gly Lys Leu Ser Lys
195 200 205

Ala Gly Ser Glu Ser Ser Ser Ser Ala Gly Ser Ser Gly Ser Leu Ser
210 215 220

Arg Thr His Pro Pro Leu Glu Ser Thr Pro Leu Val Ser Gly Val Ala
225 230 235 240

Ala Gly Ser Pro Gly Cys Val Pro Tyr Pro Glu Asn Gly Ile Gly Gly
245 250 255

Gln Val Ala Pro Ser Ser Thr Ser Tyr Ile Leu Leu Pro Leu Glu Ala
260 265 270

Ala Thr Gly Ile Pro Pro Gly Ser Ile Leu Leu Asn Pro His Thr Gly
275 280 285

Gln Pro Phe Val Asn Pro Asp Gly Thr Pro Ala Ile Tyr Asn Pro Pro
290 295 300

Thr Ser Gln Gln Pro Leu Arg Ser Ala Met Val Gly Gln Ser Gln Gln
305 310 315 320

Gln Pro Pro Gln Gln Gln Pro Ser Pro Gln Pro Gln Gln Val Gln
325 330 335

Pro Pro Gln Pro Gln Met Ala Gly Pro Leu Val Thr Gln Ser Val Gln
340 345 350

Gly Leu Gln Ala Ser Ser Gln Ser Val Gln Tyr Pro Ala Val Ser Phe
355 360 365

Pro Pro Gln His Leu Leu Pro Val Ser Pro Thr Gln His Phe Pro Met
370 375 380

Arg Asp Asp Val Ala Thr Gln Phe Gly Gln Met Thr Leu Ser Arg Gln
385 390 395 400

Ser Ser Gly Glu Thr Pro Glu Pro Pro Ser Gly Pro Val Tyr Pro Ser
405 410 415

Ser Leu Met Pro Gln Pro Ala Gln Gln Pro Ser Tyr Val Ile Ala Ser
420 425 430

Thr Gly Gln Gln Leu Pro Thr Gly Gly Phe Ser Gly Ser Gly Pro Pro
435 440 445

16U 100 PCT.ST25
 Ile Ser Gln Gln Val Leu Gln Pro Pro Pro Ser Pro Gln Gly Phe Val
 450 455 460

Gln Gln Pro Pro Pro Ala Gln Met Pro Val Tyr Tyr Tyr Pro Ser Gly
 465 470 475 480

Gln Tyr Pro Thr Ser Thr Thr Gln Gln Tyr Arg Pro Met Ala Pro Val
 485 490 495

Gln Tyr Asn Ala Gln Arg Ser Gln Gln Met Pro Gln Ala Ala Gln Gln
 500 505 510

Ala Gly Tyr Gln Pro Val Leu Ser Gly Gln Gln Gly Phe Gln Gly Leu
 515 520 525

Ile Gly Val Gln Gln Pro Pro Gln Ser Gln Asn Val Ile Asn Asn Gln
 530 535 540

Gln Gly Thr Pro Val Gln Ser Val Met Val Ser Tyr Pro Thr Met Ser
 545 550 555 560

Ser Tyr Gln Val Pro Met Thr Gln Gly Ser Gln Gly Leu Pro Gln Gln
 565 570 575

Ser Tyr Gln Gln Pro Ile Met Leu Pro Asn Gln Ala Gly Gln Gly Ser
 580 585 590

Leu Pro Ala Thr Gly Met Pro Val Tyr Cys Asn Val Thr Pro Pro Thr
 595 600 605

Pro Gln Asn Asn Leu Arg Leu Ile Gly Pro His Cys Pro Ser Ser Thr
 610 615 620

Val Pro Val Met Ser Ala Ser Cys Arg Thr Asn Cys Ala Ser Met Ser
 625 630 635 640

Asn Ala Gly Trp Gln Val Lys Phe
 645

<210> 55
 <211> 651
 <212> PRT
 <213> Homo sapien

<400> 55

Arg Asp Arg Met Ile Leu Leu Lys Met Glu Gln Glu Ile Ile Asp Phe
 1 5 10 15

Ile Ala Asp Asn Asn Asn His Tyr Lys Lys Phe Pro Gln Met Ser Ser
 20 25 30

Tyr Gln Arg Met Leu Val His Arg Val Ala Ala Tyr Phe Gly Leu Asp
 35 40 45

His Asn Val Asp Gln Thr Gly Lys Ser Val Ile Ile Asn Lys Thr Ser
 50 55 60

Ser Thr Arg Ile Pro Glu Gln Arg Phe Cys Glu His Leu Lys Asp Glu
 65 70 75 80

16U 100 PCT.ST25

Lys Gly Glu Glu Ser Gln Lys Arg Phe Ile Leu Lys Arg Asp Asn Ser
85 90 95

Ser Ile Asp Lys Glu Asp Asn Gln Ser Val Cys Ser Gln Glu Ser Leu
100 105 110

Phe Val Glu Asn Arg Leu Leu Glu Asp Ser Asn Ile Cys Asn Glu Thr
115 120 125

Tyr Lys Lys Arg Gln Leu Phe Arg Gly Asn Arg Asp Gly Ser Gly Arg
130 135 140

Thr Ser Gly Ser Arg Gln Ser Ser Ser Glu Asn Glu Leu Lys Trp Ser
145 150 155 160

Asp His Gln Arg Ala Trp Ser Ser Thr Asp Ser Asp Ser Ser Asn Arg
165 170 175

Asn Leu Lys Pro Ala Met Thr Lys Thr Ala Ser Phe Gly Gly Ile Thr
180 185 190

Val Leu Thr Arg Gly Asp Ser Thr Ser Ser Thr Arg Ser Thr Gly Lys
195 200 205

Leu Ser Lys Ala Gly Ser Glu Ser Ser Ser Ser Ala Gly Ser Ser Gly
210 215 220

Ser Leu Ser Arg Thr His Pro Pro Leu Gln Ser Thr Pro Leu Val Ser
225 230 235 240

Gly Val Ala Ala Gly Ser Pro Gly Cys Val Pro Tyr Pro Glu Asn Gly
245 250 255

Ile Gly Gly Gln Val Ala Pro Ser Ser Thr Ser Tyr Ile Leu Leu Pro
260 265 270

Leu Glu Ala Ala Thr Gly Ile Pro Pro Gly Ser Ile Leu Leu Asn Pro
275 280 285

His Thr Gly Gln Pro Phe Val Asn Pro Asp Gly Thr Pro Ala Ile Tyr
290 295 300

Asn Pro Pro Thr Ser Gln Gln Pro Leu Arg Ser Ala Met Val Gly Gln
305 310 315 320

Ser Gln Gln Gln Pro Pro Gln Gln Gln Pro Ser Pro Gln Pro Gln Gln
325 330 335

Gln Val Gln Pro Pro Gln Pro Gln Met Ala Gly Pro Leu Val Thr Gln
340 345 350

Ser Val Gln Gly Leu Gln Ala Ser Ser Gln Ser Val Gln Tyr Pro Ala
355 360 365

Val Ser Phe Pro Pro Gln His Leu Leu Pro Val Ser Pro Thr Gln His
370 375 380

Phe Pro Met Arg Asp Asp Val Ala Thr Gln Phe Gly Gln Met Thr Leu
385 390 395 400

160 100 PCT.ST25

Ser Arg Gln Ser Ser Gly Glu Thr Pro Glu Pro Pro Ser Gly Pro Val
405 410 415

Tyr Pro Ser Ser Leu Met Pro Gln Pro Ala Gln Gln Pro Ser Tyr Val
420 425 430

Ile Ala Ser Thr Gly Gln Gln Leu Pro Thr Gly Gly Phe Ser Gly Ser
435 440 445

Gly Pro Pro Ile Ser Gln Gln Val Leu Gln Pro Pro Pro Ser Pro Gln
450 455 460

Gly Phe Val Gln Gln Pro Pro Pro Ala Gln Met Pro Val Tyr Tyr Tyr
465 470 475 480

Pro Ser Gly Gln Tyr Pro Thr Ser Thr Thr Gln Gln Tyr Arg Pro Met
485 490 495

Ala Pro Val Gln Tyr Asn Ala Gln Arg Ser Gln Gln Met Pro Gln Ala
500 505 510

Ala Gln Gln Ala Gly Tyr Gln Pro Val Leu Ser Gly Gln Gln Gly Phe
515 520 525

Gln Gly Leu Ile Gly Val Gln Gln Pro Pro Gln Ser Gln Asn Val Ile
530 535 540

Asn Asn Gln Gln Gly Thr Pro Val Gln Ser Val Met Val Ser Tyr Pro
545 550 555 560

Thr Met Ser Ser Tyr Gln Val Pro Met Thr Gln Gly Ser Gln Gly Leu
565 570 575

Pro Gln Gln Ser Tyr Gln Gln Pro Ile Met Leu Pro Asn Gln Ala Gly
580 585 590

Gln Gly Ser Leu Pro Ala Thr Gly Met Pro Val Tyr Cys Asn Val Thr
595 600 605

Pro Pro Thr Pro Gln Asn Asn Leu Arg Leu Ile Gly Pro His Cys Pro
610 615 620

Ser Ser Thr Val Pro Val Met Ser Ala Ser Cys Arg Thr Asn Cys Ala
625 630 635 640

Ser Met Ser Asn Ala Gly Trp Gln Val Lys Phe
645 650

<210> 56
<211> 89
<212> PRT
<213> Homo sapien

<400> 56

Met Ser Glu Gln Gly Asp Leu Asn Gln Ala Ile Ala Glu Glu Gly Gly
1 5 10 15

Thr Glu Gln Glu Thr Ala Thr Pro Glu Asn Gly Ile Val Lys Ser Glu
20 25 30

16U 100 PCT.ST25

Ser Leu Asp Glu Glu Glu Lys Leu Glu Leu Gln Arg Arg Leu Glu Ala
 35 40 45

Gln Asn Gln Glu Arg Arg Lys Ser Lys Ser Gly Ala Gly Lys Gly Lys
 50 55 60

Leu Thr Arg Ser Leu Ala Val Cys Glu Glu Ser Ser Ala Arg Pro Gly
 65 70 75 80

Gly Glu Ser Leu Gln Asp Gln Thr Leu
 85

<210> 57
 <211> 88
 <212> PRT
 <213> Mus musculus

<400> 57

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